

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 00:35:15 ; Search time 11362 Seconds
(without alignments)
12452.463 Million cell updates/sec

Title: US-10-692-556-1
Perfect score: 3717
Sequence: 1 atgttttgccgcggcggg.....ccttgatacttagcatga 3717

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	146	3.9	689	AG126971	Pan trogl
C 2	124.2	3.3	650	AG061486	Pan trogl
C 3	123.4	3.3	673	AG131496	Pan trogl
C 4	95.4	2.6	706	AG049882	Pan trogl
C 5	90.4	2.4	645	AJ723867	Pan trogl
C 6	89	2.4	724	AG826841	Pan trogl
C 7	89	2.4	1038	BE332861	Pan trogl
C 8	86.4	2.3	503	BE35321	Pan trogl
C 9	85.4	2.3	925	BE350425	Pan trogl
C 10	84.8	2.3	1368	BQ053856	Pan trogl
C 11	84.6	2.3	687	B1118205	Pan trogl
C 12	84.2	2.3	727	AJ723868	Pan trogl
C 13	82.2	2.2	1956	CG754548	Pan trogl
C 14	82	2.2	453	BP096735	Pan trogl
C 15	81.6	2.2	1009	CNS010EM	Pan trogl
C 16	81.2	2.2	622	BQ743697	Pan trogl
C 17	79.8	2.1	347	CK234399	Pan trogl
C 18	79.8	2.1	834	BE737103	Pan trogl
C 19	77.4	2.1	1035	BQ071299	Pan trogl
C 20	76.4	2.1	917	CR633636	Pan trogl
C 21	76.4	2.1	1398	CR716960	Pan trogl
C 22	75.4	2.0	462	B1344718	Pan trogl
C 23	75.4	2.0	1083	CK206171	Pan trogl
C 24	74.8	2.0	998	BQ881418	Pan trogl

25	74.6	2.0	541	2	BE013096	BE013096 122887 MA
C 26	74.4	2.0	925	9	CNS0091P	AL053013 Drosophil
C 27	73.6	2.0	581	4	BG145187	BG145187 uc76909.y
C 28	73.6	2.0	712	6	CD372246	CD372246 UI-R-G00-
C 29	73.6	2.0	923	5	BUS14091	BUS14091 AGENCOURT
C 30	73.6	2.0	3409	3	AK088310	AK088310 Mus muscu
C 31	73.4	2.0	568	2	BF203965	BF203965 601868975
C 32	73.4	2.0	788	2	BF205093	BF205093 601868825
C 33	73.2	2.0	1628	9	CG757066	CG757066 P052-2-A0
C 34	72.8	2.0	925	9	CNS0091P	AL053013 Drosophil
C 35	72.6	2.0	699	9	BX906960	BX906960 Leishmani
C 36	72.6	2.0	699	9	LBAF026G07	BX544067 Leishmani
C 37	72.6	2.0	684	8	AQ163340	AQ163340 mgxb0023L
C 38	71.2	1.9	371	2	BF292456	BF292456 WHE2214.A
C 39	71.2	1.9	953	5	BQ232039	BQ232039 AGENCOURT
C 40	70.6	1.9	1509	9	CL959255	CL959255 OsIFCC002
C 41	70	1.9	1002	9	AG046242	AG046242 Pan trogl
C 42	69.6	1.9	798	4	BM044191	BM044191 603621433
C 43	69.6	1.9	876	4	BM048573	BM048573 603623915
C 44	69.4	1.9	699	6	CD371733	CD371733 UI-R-G00-
C 45	69	1.9	935	9	CNS0065XK	AL066051 Drosophil

ALIGNMENTS

RESULT 1	AG126971/c	AG126971	Pan troglodytes DNA, clone: PTB-137L02.F, genomic survey sequence.	689 bp	DNA	linear	GSS 04-NOV-2001
LOCUS	AG126971	AG126971					
DEFINITION	AG126971	AG126971					
ACCESSION	AG126971	AG126971					
VERSION	AG126971.1	GI:16656136					
KEYWORDS	GSS						
SOURCE	Pan troglodytes (chimpanzee)						
ORGANISM	Pan troglodytes						
REFERENCE	1	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.					
AUTHORS	1	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.					
TITLE	Unpublished						
JOURNAL	BAC end sequences of Library PTB						
REFERENCE	2	(bases 1 to 689)					
AUTHORS	1	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.					
TITLE	Submitted (02-AUG-2001)						
JOURNAL	Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsukuba, Ibaraki, Japan, 305-8565, Japan (E-mail: chimbes@sc.riken.go.jp, Fax: 81-45-503-9170) Tel: 81-45-503-9111, URL: http://hgp.gsc.riken.go.jp/.						
COMMENT	Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.						
PRIMERS	Sequencing: -21m13						
LIBRARY	Vector : pKS145						
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	R.Site 2 : SacI						
FEATURES	Location/Qualifiers						
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	/mol_type="genomic DNA"						
	/db_xref="taxon:9598"						
	/clone="PTB-137L02.F"						
	/sex="male"						
	/cell_type="lymphoblast"						
	/clone_lib="PTB Chimpanzee Male BAC Library"						
ORIGIN							
Query Match	3.9%						
Best Local Similarity	57.5%						
	Score 146;						
	DB 9;						
	Length 689;						
	Pred. No. 7.8e-18;						


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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
REFERENCE
2 (bases 1 to 673)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
LIBRARY
Sequencing: M13Rev
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-143J08.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN
Query Match 3.3%; Score 123.4; DB 9; Length 673;
Best Local Similarity 56.2%; Pred. No. 1.8e-13;
Matches 232; Conservative 0; Mismatches 181; Indels 0; Gaps 0;
QY 2650 CGCATCATCTACGGGACACGACTCCATTTTGTGTCGCGGCTCATCGGCGCG 2709
Db |||||
QY 518 CGAGTCATGTACGGGACACGACTCTCTGTTTATCGATGGCGGGGTTTTCAGAGAGC 459
Db |||||
QY 2710 GCCTGTGTCATGGGACACAGATGGGAGCCACATCTCGGCGCGTGTCTCCGC 2769
Db |||||
QY 458 GAGACCTCGCTTGGCCATCGCTGGCGCGCCACACCGCGAGCCGTGTGTGGCC 399
Db |||||
QY 2770 CCGATCAAGCTCGAGTGCAGAAACGTTTACCAAGCTGCTCATGSCCAAGAAAG 2829
Db |||||
QY 398 CCATCTCGCTGAGCCGAGAGACCTTCTCTGCTGATGCTGATTACAAAGAGAGA 339
Db |||||
QY 2830 TACATGGCGCTCATTCGCGGGGCAAGATGCTCATCAAGGGCGTGGATCTGGTGGC 2889
Db |||||
QY 338 TATGTGGGGTGTCTGACGAGCGCAAGACCTGTATGAAGGGGTGGAGCTCGTCCG 279
Db |||||
QY 2890 AACAACTGGCGTTTATCAACCGACCTTCAGGGCGCTGTCAGCTGCTGTTTACGAC 2949
Db |||||
QY 278 ACGGCTTCAAGTTTGTGCAGACACGCTGCGCGCGTGTCTGACCTGTGTGCGGAT 219
Db |||||
QY 2950 GATACCGTATCCGAGCGCGCCCGCTTGTAGCCGAGCGCCCGCAGAGAGTGGTGGCG 3009
Db |||||
QY 218 GCCCGGTTAAGAGCGCGCAGCTCTCTCCACCGGCCCTTCCAGAGATCAATTACA 159
Db |||||
QY 3010 CGACCCCTGCGCGAGGAGCTGAGGCGTTTGGGGCGCTCTCGTAGAGCCCA 3062
Db |||||
QY 158 CAAGGGCTACCTGTGGGCTTTTGGCCGTCATTGACATCTTAAACACGCGCTA 106
Db |||||

RESULT 4
AG049882/c 706 bp DNA linear GSS 02-NOV-2001
LOCUS Pan troglodytes DNA, clone: PTB-030C07.R, genomic survey sequence.
DEFINITION
ACCESSION AG049882
VERSION AG049882.1 GI:16586774
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
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Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 706)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
LIBRARY
Sequencing: M13Rev
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-030C07.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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Best Local Similarity 53.1%; Pred. No. 4.7e-08;
Matches 249; Conservative 0; Mismatches 216; Indels 4; Gaps 2;
QY 2412 CCTCTCGACAAACAGCGCGCATCAAGTGGTGTGCAACTCGGTGTACGGGTTCAC 2471
Db |||||
QY 580 CATCCATTTTCAACAAACAGTTGACCATCAAGTGCAGTGCATCGCGTAAATCGGTTCCAC 521
Db |||||
QY 2472 CGGGCGGACGACGCTTCTTCCCTGCTGCACTGGCGGCCACCGTGACACCAATCGG 2531
Db |||||
QY 520 CGGGGTGGCCAAACGCGCTTTTCCCTCTGACCAATTATCAAGTTGGTAACTTTGCAGGT 461
Db |||||
QY 2532 CCGCG-AGATGCTCTCGCGACGCGGTAGTGCACGCGCTGGCGGAGTTTCGATC 2590
Db |||||
QY 460 CGCTTATATGTTGGAGCGGACCAAGGCTTCTGTAAGTCCATAAACCCGCAACTTCG 401
Db |||||
QY 2591 AGCTGTGCGCACTTTTCCGGAGGCGCGCGCATCGGCGCCCGCTCGTACTCCATCG 2650
Db |||||
QY 400 AGGCTTGGCCCTCCCGTACGTTTGGCGGCCCTCATCACCGA---GGGCCAGCTTT 344
Db |||||
QY 2651 GCATCATCTAGCGGACAGGACTCCATTTTGTGTCGCGCGCTCAGCGCGCGG 2710
Db |||||
QY 343 GAGTCATATACGGGAACACGTACTCACTGTTTATTGAGTGGCGGGGTTTTCAGAGAACG 284
Db |||||
QY 2711 GCCTGTGGCCATGGCGCAAGAATGGCGAGCCACATCTCGCGCGCTGTTCTCCGCC 2770
Db |||||
QY 283 AGACCTGGCTTTGCCAATGCCCTGTCCGCCACACACCGGAGCTTTTGTGGCCC 224
Db |||||
QY 2771 CGATCAAGCTCGAGTGCAGAAACAGTTTCAACAGCTGCTGCTATCCCAAGAAAAAGT 2830
Db |||||
QY 223 CCATCTCCCTGAAGACCGAGAAGACCTTCTCTGCTGATCTGATTACAAGAAGAGAT 164
Db |||||
QY 2831 ACATCGGCGTATCTGCGGGGCGAAGATGCTCATCAAGGGCGTGGATCT. 2879
Db |||||
QY 163 ATGTGGGGGTGCTGACGACGCGCAAGACCTGATTAAAGGGGTGTAGCT 115
Db |||||
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```
RESULT 5
AJ723867/c
LOCUS AJ723867 riken1 Gallus gallus CDNA clone 26j2284, mRNA linear EST 07-OCT-2004
DEFINITION AJ723867
ACCESSION AJ723867
VERSION AJ723867.1 GI:53889281
KEYWORDS EST
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
REFERENCE
AUTHORS Caldwell, R.B., Kierzek, A.M., Arakawa, H., Bezzubov, Y., Zaim, J.,
Fiedler, P., Kutter, S., Blagodatski, A., Kostovska, D., Koter, M.,
Plachy, J., Carninci, P., Hayashizaki, Y. and Buerstedde, J.M.
TITLE Full-length cDNAs from bursal lymphocytes to facilitate gene
function analysis
JOURNAL Unpublished (2004)
COMMENT Contact: Caldwell RB
GSF - Forschungszentrum, Institut fuer Molekulare Strahlenbiologie
Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY.
FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="26j2284"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/clone_lib="riken1"
/note="CB inbred strain"
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Query Match 2.4%; Score 90.4; DB 1; Length 645;
Best Local Similarity 50.2%; Pred. No. 4.4e-07;
Matches 254; Conservative 0; Mismatches 246; Indels 6; Gaps 1;
QY 2116 GACCCACCTCGGGTTTCAGTCGACCCCGTGGTGTGTTGACTTTGCGAGCTGTAC 2175
DB 645 GAGCCCAAGAAGGGTTACTAGAGTCCCGCCATCGCCAGTTGGACTTCAGCTCTCTGTAC 586
QY 2176 CCCAGCATCCAGGCCCCACACTGCTGTCTAGTAGCTCTCCCTCGGCCCGAGGCC 2235
DB 585 CCCTCCATTATGATGGCCCAATCTGTGTACACCACTGTGCTGCCCGCCGCGCGCG 526
QY 2236 GTCGCGCACCTGGAGCGGACCGGACTACCTGGAGATCGAGGTGGGGGGCGGACGGCTG 2295
DB 525 CAGCGCTACGGGCTGAGCCCCACGNAATTACATCCGACCCCGGAGT-----CTC 472
QY 2296 TTCTTGTGAAGGCCACGATGCGGAGAGCTGTGTAGCATCTGTCTGCGGAGCTGGCTG 2355
DB 471 TTTGTGACGGGGCGGTGCGCGTGGGCTGTGCCCCGCATCTCGAGGGGCTGTGGCG 412
QY 2356 GCCATGCCAAGACAGATCCGCTCGCGGATCCCCAGACACCCCGAGGAGCGCTCTCTC 2415
DB 411 GCGGGCCGACGGGCAAGAGAGAGTGTGCGGGAGACGGACCCGTTTCCGCGCTCATGTC 352
QY 2416 CTCGACAAAGCAACAGCGGCCCATCAAGGTGGTGTGCAACTCGGTGTACGGGTTCACCGGG 2475
DB 351 CTGAGCGCGCGGAGATGCGCTCAAAGTCAGCGCCAACTCCGTGTACGGCTTCACCGGG 292
QY 2476 GCGAGCAACGGTCTTCTGCGCTGCTGCACTGCGCGCGCCACCGTGACCAACATCGGCGCG 2535
DB 291 GCGAGGCGGGGGCGGCTCCCGTGCCTCGAGATCTCGCAGAGCGTGACGGGGTTGCGGCGG 232
QY 2536 GAGATGCTCTCCGCGACGCGCGGTACGTGCACGCGCGCTGCGGCGAGTTTCGATCAGCTG 2595
DB 231 CAGATGATTGAGCGCACGACCAATTGGTGAGTGCACCTTCTGTGTGGCAATGGGTAC 172
QY 2596 GTGCGCGACTTTTCGGAGCGCGCGG 2621
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DB 171 CCCGGGACGCCAAGGTGGTGACGG 146
RESULT 6
BG826841
LOCUS BG826841
DEFINITION 602750915F1 NIH_MGC_17 Homo sapiens CDNA clone IMAGE:4903851 5',
mRNA sequence.
ACCESSION BG826841
VERSION BG826841.1 GI:14174428
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI802 row: m column: 04
High quality sequence stop: 724.
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/clone="IMAGE:4903851"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_17"
/note="Organ: muscle; Vector: pOTB7; Site 1: EcoRI;
Site 2: XhoI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

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ORIGIN
Query Match 2.4%; Score 89; DB 4; Length 724;
Best Local Similarity 51.5%; Pred. No. 8.2e-07;
Matches 262; Conservative 0; Mismatches 235; Indels 12; Gaps 2;
QY 2039 AGGACGGGACGACGCGAGGAGTCCGCGCGGAGACCGGGGGCGGCGACGCTTGGGTACC 2098
DB 15 AGGCCATGACGAGGGGCTGCTGATGCGGTGGAAGTCAGAGGGCGGCGAGACTACA 74
QY 2099 AGGGGGCCGGGTCCCTCGACCCCACTCCGGGTTTCAGTCCACCCCGTGGTGTGTTG 2158
DB 75 CGGAGGCCACTGTTCATCGAGCCCTCAAAGGGTACTACGACGTCCCATGCCACCTGG 134
QY 2159 ACTTTGCGAGCTGTACCCAGCATCATCCAGGCCACACACCTGCTTTCAGTAGGCTCT 2218
DB 135 ACTTCTCTCGCTGTATCCCGTCCATCATGATGGCCCCAACCTGTGTTTACACCGCTCC 194
QY 2219 CCCTGCGGCCCGAGGCGCTGCGCACCTTGGAGGGCGGACCGGGACTACCTGAGATCGAGG 2278
DB 195 TTCGGC-----CCGGGACTGCACAGAACTGGGCTGACTGAGGATCAGTTTCATCA 245
QY 2279 TGGGGGGCGGACGGCTGTTCTTTCGTGAAGGCCCACTGACGCGGAGAGCGCTGTGAGCATCC 2338
DB 246 GGACCCCGACCGGGGACGAGTTTGTGAAGACTCTCAGTCCGGAAGGGGTCTGTGCCCCAGA 305
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QY 2339 TGTGCGCACTGTGGTGGCCATCGGAAGCAGATCCGCTCGCGGATCCCCAGAGCAC-- 2396
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 Db 306 TCTTGAGAACCTGTCTAGTGCCTCCGAGAGGCCAAGGCCGAGCTGGCCAGGAGACAG 365
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 QY 2397 -CCCGAGAGAGCGCTCTCTCTCGACAGACAGAGCCGCCATCAAGTGTGTGCAACT 2455
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 Db 366 ACCCCCTCCGGCCACAGGCTCTGGATGGACGGCAGCTGGCTGGAAGGTGAGCGCAACT 425
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 QY 2456 CGGTGTACGGGTTCACCGGGGGCGACACGGTCTTCTGCGCTGCTGCTGACAGTGGCGGCA 2515
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 Db 426 CCGTATACGGCTTCACTGGCGCCAGGTGGGCAAGTGGCTGCGCTGGAGATCTACAGA 485
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 QY 2516 CCGTGACAGACCATCGGCCCGGAGATGCTC 2544
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 Db 486 GCGTCACGGGGTTCGAGCTCAGATGATC 514
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RESULT 7

LOCUS BX382861
 DEFINITION BX382861 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
 Homo sapiens cDNA clone CS0DJ001YC08 5-PRIME, mRNA sequence.
 ACCESSION BX382861
 VERSION BX382861.2 GI:46833596
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1038)
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 8, 2003 this sequence version replaced gi:30459096.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 9280.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS0DJ001BB04QPl&c=9280.f.

FEATURES

source
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 /cell_line="JURKAT"
 /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
 ORIGIN

Query Match 2.4%; Score 89; DB 5; Length 1038;
 Best Local Similarity 51.5%; Pred. No. 8.2e-07;
 Matches 262; Conservative 0; Mismatches 235; Indels 12; Gaps 2;
 QY 2039 AGGACGGGACGAGCGGAGGAGTCCGCGGAGACCGGGGGCGGACGCTGGGTACC 2098
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 Db 172 AGGCCATGACAGAGGGGCTGTGTATGATCCCGTGTGAATGTCAGAGGCGCGGAGGACTACA 231
 |||||
 QY 2099 AGGGGGCGGGTCTCGACCCACCTCGGGTTTCAGTGCACCCCGTGGTGGTTG 2158
 |||||
 Db 232 CGGGAGCCACTGTCTATCGAGGCCCTCAAAGGGGTACTACGACGTCCTCCCATCGCCACCTGG 291
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QY 2159 ACTTTGCCAGCCTGTATACCCAGCATCATCCAGGCCCAACAACCTGTGCTTCTAGTAGCTCT 2218
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 Db 292 ACTTCTCTCGCTGTATCCCGTCCATCATGATGGCCCAACAACCTGTGTTACACAGCTCC 351
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 QY 2219 CCGTGGGCCCGGAGCGCTCGCGCACCTGGAGCGGACCGGACTACCTGGAGATCGAGG 2278
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 Db 352 TTCCGCG-----CCGGGACTGCACAGAAACTGGGCTGACTGAGGATCACTTTCATCA 402
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 QY 2279 TGGGGGGCGGAGCGGCTGTCTTCGTGAAGGCCACAGTACGCGAGAGCGCTGCTGAGCATCC 2338
 |||||
 Db 403 GACCCCCCACCAGGGGAGCAGAGTTTGTGAAGACCTCAGTGCAGAAAGGGGCTGCTGCCCCAGA 462
 |||||
 QY 2339 TGTGCGCGCACTGGCTGGCCATCGGAAGCAGATCCGCTCGCGGATCCCCAGAGCAC-- 2396
 |||||
 Db 463 TCCTGGAGAACCTGCTCAGTGCCTCGGAGAGGGCCAGGCCGAGTGGCCAGGAGACAG 522
 |||||
 QY 2397 -CCCGAGAGGCGCTCTCTCTCGACAAGCAACAGCGGCCCATCAAGTGTGTGCAACT 2455
 |||||
 Db 523 ACCCCCTCCGGTGCAGGCTCTGGATGGACGGCAGCTGGCGTGAAGGTGAGCGGCAACT 582
 |||||
 QY 2456 CGGTGTACGGGTTCACCGGGGGCGGAGCAGCGTCTTCTGCGCTGCTGCGCTGCGCGCCA 2515
 |||||
 Db 583 CCGTATACGGCTTCACTGCGGCCCGAGGTGGGCAAGTTGCCGCTGGAGATCTCACAGA 642
 |||||
 QY 2516 CCGTGACGACCATCGGCCCGGAGATGCTC 2544
 |||||
 Db 643 GCGTCACGGGGTTCGAGCTCAGATGATC 671
 |||||

RESULT 8

LOCUS BE535321
 DEFINITION 601058865F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445168 5',
 mRNA sequence.
 ACCESSION BE535321
 VERSION BE535321.1 GI:9763966
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 503)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 plate: L1AM8415 row: b column: 17
 High quality sequence stop: 503.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3445168"
 /cell_line="MGC36"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_10"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.5 kb. Library prepared by Life
 Technologies."

FEATURES

source
 1..503
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3445168"
 /cell_line="MGC36"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_10"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.5 kb. Library prepared by Life
 Technologies."

ORIGIN

Query Match 2.3%; Score 86.4; DB 2; Length 503;

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Best Local Similarity 52.6%; Pred. No. 2.6e-06;
Matches 242; Conservative 0; Mismatches 206; Indels 12; Gaps 2;

QY 2088 GCTGGGTACAGGGGGCCGGGCTCTCGACCCACCTCCGGGTTTCAGTCGACCCCGT 2147
Db 21 CGAGGACTACAGGGAGCCACTGTCTATCGAGCCCTCAAGGGTACTACGACGTCCTCCCAT 80

QY 2148 GGTGGTGTGACITTTGTCAGGCTGTATCCCGCAGCATCATCCAGGCCCAACCTGTGCTT 2207
Db 81 CGCCACCTGGACTTCTCTCGCTGTATCCCGTCCATCATGTATGGCCCAACACCTGTGTTA 140

QY 2208 CAGTACGCTCTCCCTGCGGCCCGAGGCGTCCGCGACCTCGAGGCGGACCGGACTACCT 2267
Db 141 CACACGCTCTCTCGGC-----CCGGACTGCACAGAAACTGGGCCCTGACTGAGGA 191

QY 2268 GGAGATCAGGTGGGGGCGCAGCGCTGTTCTTGTGAAGGCCCAACGCTTACGCGAGAGCCT 2327
Db 192 TCAGTTTCATCAGGACCCCGGAGCGAGTGTGTGAAGACCTCAGTGCAGGAGGGGCT 251

QY 2328 GCTGAGCATCTGTCGCGACTGGCTGGCCATCGGAAGCAGATCCGCTCGCGATCCC 2387
Db 252 GCTGCCCCAGATCTCTGGAGAACCTGCTCAGTGCCTCGGAGAGGGCCAAAGGCGGAGCTGGC 311

QY 2388 CCAGAGCAC---CCCCGAGGAGGCGCTCTCTCTGACAAAGCAACAGGCGCGCATCAAGGT 2444
Db 312 CAAGGAGACACCCCTCCGCGCCAGGTCTCTGATGGACGGCAGCTGGCGCTGAGGT 371

QY 2445 GGTGTGCAACTCGGTGTACGGGTTACCGGGGCGCAGCAGCGTCTTTCGCCCTGCCGTGA 2504
Db 372 GAGCGCCAACTCCGTATACGGCTTCACTGGGCGCCAGGTGGGCAAGTTGCCGTGCTTGA 431

QY 2505 CGTGCGCCGCCACCGTGAGCAACATCGGCGCGAGATGCTC 2544
Db 432 GATCTCAGACGCGTCACGGGTTTCGGACGTCAGATGATC 471
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RESULT 9
BX350425/c
LOCUS BX350425 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
DEFINITION cDNA clone CS0DK004YH13 3-PRIME, mRNA sequence.
ACCESSION BX350425
VERSION BX350425.2 GI:46550868
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 925)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30379510.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9280.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BA1036ZG10_CS03439_1&c=9280.f
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FEATURES
source
1. 925
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK004YH13"
/cell_type="HELA CELLS COT 25-NORMALIZED"
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/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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ORIGIN

```
Query Match 2.3%; Score 85.4; DB 5; Length 925;
Best Local Similarity 50.9%; Pred. No. 4.1e-06;
Matches 259; Conservative 0; Mismatches 238; Indels 12; Gaps 2;

QY 2039 AGGACGGGGACGAGCGAGGAGGTCCGCGCGAGACCGGGGGCCGACGCTTCGGGTACC 2098
Db 806 AGGCATGTCAGCGAGGGGNTGCTGATGCCGCTGAGTGAAGTCAAGGNGCGGAGGACTACA 747

QY 2099 AGGGGGCCCGGGTCTCTCGACCCCACTCCCGGGTTTACGTCGACCCCGTGTGTGTTG 2158
Db 746 CGGAAGCCACTGTCTATTTGAGCCCTCAAGGGTACTACGAGCTCCCATCGCCACCTGG 687

QY 2159 ACTTTGCCAGCTGTATCCCGCAGCATATCCAGGCCCAACACTGTGTTCAGTACGCTCT 2218
Db 686 ACTTCTCTCGCTGTACCCCGTCCATCATGTATGGCCCAACACTGTGTGTACACCACTCC 627

QY 2219 CCCTGCGGCCCGAGGGCGCTCGCGCACCTGGAGGGCGGACCTACTCTGGAGATCGAGG 2278
Db 626 TTCGGC-----CCGGACTGCACAGAAACTGGGCCCTGACTGAGGATCAGTTCA 576

QY 2279 TGGGGGGCCGACGCGCTGTTCTTGTGAAGGCCCAACGCTACGCGAGAGCTGTCTGAGCATCC 2338
Db 575 GGACCCCCACCGGGGACGAGTTTGTGAAGACCTCAGTGCAGAGGGGCTGTGTCGCCAGA 516

QY 2339 TGCTGCGCGACTGTGTCGCGCATGCGAAAGCAGATCCCGCTCGCGGATCCCCCAGAGCAC-- 2396
Db 515 TCCTGGAGAACCTGCTCAGTGCCTCGGAGAGGGGCAAGGCGGACCTGCGCCAAAGAGACAG 456

QY 2397 -CCCCGAGGAGGCGCTCTCTCTGACAAAGCAACAGGCGCGCATCAAGTGTGTGCAACT 2455
Db 455 ACCCTCTCGGCGCAGCTCTCTGATGGACGGCAGCTGGCGCTGAAGGTGAGCGCCAACT 396

QY 2456 CGGTGTACGGGTTACCGGGGCGCAGCACCGTCTTCTGCCCTGCTGTGACGTGCCGCCA 2515
Db 395 CCGTATACGGCTTCACTGGGCGCCAGGTGGGCAAGTTGCCGTGCTGTGAGATCTCACAGA 336

QY 2516 CCGTGACGACCATCGGCGCGAGATGCTC 2544
Db 335 CGGTACCGGGTTCCGGACGTCAGATGATC 307
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RESULT 10
BX053856
LOCUS BX053856
DEFINITION AGENCOURT 6874222 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5935767
5', mRNA sequence.
ACCESSION BX053856
VERSION BX053856.1 GI:19813196
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1368)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Ruben Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
```

http://image.llnl.gov
Plate: LLCM2124 row: a column: 16
High quality sequence stop: 219.
Location/Qualifiers

FEATURES

source

1..1368
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5935767"
/tissue_type="natural killer cells, cell line"
/lab_host="PH10B (phage-resistant)"
/clone_lib="NIH_MGC_106"
/note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 2.3%; Score 84.8; DB 5; Length 1368;
Best Local Similarity 52.1%; Pred. No. 5.4e-06;
Matches 239; Conservative 0; Mismatches 202; Indels 13; Gaps 2;
QY 2096 ACCAGGGGCGGGTCTCGACCCACCTCCGGGTTTCACGTGACCCCGTGGTGT 2155
DB 1 ACACGGAGCCACTGTCTGACGCGCTCAAGGGTACTACGACGTCCCATCGCCACC 60
QY 2156 TTGACTTGGCCAGCTGTACCCAGCATCATCAGGCCACCACTGTCTTCAGTACGC 2215
DB 61 TGGACTTCTCTCTGTACCCGTCATCATGATGCCCCACAACTGTGTACACACGC 120
QY 2216 TCTCTCGGGCCGAGGCGCTGCGACCTGGAGCGGACCGGACTACCTGGAGATCG 2275
DB 121 TCTTTCGGC-----CCGGGACTGCACAGAACTGGGCTGACTGAGGATCATGTTCA 171
QY 2276 AGGTGGGGGGCGAGCGGTGTTCTTGTGAAGGCCACGTACGCGAGAGCCTGTGAGCA 2335
DB 172 TCATGACCCCAACCGGGAGAGTTTGTGAAGACTCATGTGCGAAGGGGTGCTGCCCC 231
QY 2336 TCTCTGTGCGCACTGTGTGGCCATGCGAAAGCAGATCGCTGCGGATGCCCCAG---- 2391
DB 232 AAATCTTGAGAACCTGTCTAGTGC CGAAGAGGCGCAAGCCGAGCTGGCCAAAGGAGA 291
QY 2392 AGCAGCCCGAGGAGCGCTCTCTCGACAGCAACAGCGCGCCATCAAGTGTGTGTC 2451
DB 292 CAGACCCCTCCGGCGCCAGGTCTCTGATGGACCGGACGTGGCGCTGAAAGGTGAGCGCC 351
QY 2452 AACTCGGTGTACGGTTTACCGGGCGCAGCAGCGTCTTCTGCCCTGCTGCACTGGCC 2511
DB 352 AACTCGTATACGGTTTACTGGCCCGCCAGGTGGGCAAGTTGCCGTCTGGAGATCTCC 411
QY 2512 GCCACCGTGACGACCATCGCCCGGAGATGCTCC 2545
DB 412 CACAGCGTCACGGGTTCCGACGTCAGATGATCC 445

RESULT 11

Bi118205
LOCUS 602867491F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:5015830 5',
DEFINITION mRNA sequence.
ACCESSION Bi118205
VERSION Bi118205.1 GI:14569106
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 687)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE JOURNAL COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1825 row: f column: 23
High quality sequence stop: 674.
Location/Qualifiers

FEATURES

source

1..687
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5015830"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 2.3%; Score 84.6; DB 4; Length 687;
Best Local Similarity 51.1%; Pred. No. 5.8e-06;
Matches 257; Conservative 0; Mismatches 234; Indels 12; Gaps 2;
QY 2039 AGGACGGGGACGAGCGGAGGAGGTGCGCGCGAGACCGGGGCGCGCATCGTTGGGTACC 2098
DB 134 AGGCATCATCAGGAGGGCTGTGATGCCGTGAAGTCAGAGGCGCGAGGACTACA 193
QY 2099 AGGGGGCGGGTCTCGACCCACCTCGGGTTTACGTGACGCCCGCTGGTGGTGTG 2158
DB 194 CGGAGGCCACTGTCTATCGAGCCCTCAAAGGGTACTACGACGTCCCATCGCCACCCCTGG 253
QY 2159 ACTTTGCGCAGCTGTACCCAGCATCTCAGGCCCAACCTGTGTCTTCACTAGCTCT 2218
DB 254 ACTTCTCTCGTGTATCCCGTCCATCATGATGGCCCAACCTGTGTACACCACTCTCC 313
QY 2219 CCTGCGGCCCGGCGCGCTCGCGCACCTGGAGGGCGGACCGGACTACCTGGAGATCGAGG 2278
DB 314 TTGGGC-----CCGGGACTGCACAGAACTGGGCTGACTGAGGATCAGTTTCATCA 364
QY 2279 TGGGGGGCGGAGCGGTGTTCTTGTGAAGGCCACGTAAGGAGAGCGCTGTGAGCATCC 2338
DB 365 GGACCCCCACCGGGGACGAGTTTGTGAAGACCTCAGTGCGAAGGGGTGCTGCCCCAGA 424
QY 2339 TGCTGCGGAGCTGGCTGSCCATGCGAAGACAGATCCGCTCGCGGATCCCCAGAGAC-- 2396
DB 425 TCCTGGAGAACCTGCTCAGTGC CGAAGAGGGCCAGCGGAGCTGGCCAAAGGAGACAG 484
QY 2397 -CCCCGAGGAGCGGTCTCTCTCGCAAGCAACAGCGCGCCCATCAAGGTGGTGTCAACT 2455
DB 485 ACCCCCTCCGGCGCGAGGTCTCTGGATGGACGCGAGCTGCGCTGAAGGTGAGCGCAACT 544
QY 2456 CGGTGTACGGGTTACCGGGGCGGACGCGGTCTTCTGCGCTGCTGACGTGGCGGCA 2515
DB 545 CCGTATACGGTTTCACTGGCGCCGAGGTGGGCAAGTTGCCGCTGCGGTGAGATCTCACAGA 604
QY 2516 CCGTGACACCATCGGCGCGAG 2538
DB 605 CGGTACCGGGGTTCCGACGTGAG 627

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RESULT 12
AJ723868/c
LOCUS AJ723868 727 bp mRNA linear EST 07-OCT-2004
DEFINITION AJ723868 riken1 Gallus gallus cDNA clone 26j22e5, mRNA sequence.
ACCESSION AJ723868
VERSION AJ723868.1 GI:53889282
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
REFERENCE 1 (bases 1 to 727)
AUTHORS Caldwell,R.B., Kierzek,A.M., Arakawa,H., Bezzubov,Y., Zaim,J.,
Archaeoaria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
Plachy,J., Kutter,S., Blagodatski,A., Kostovska,D., Kofer,M.,
Fiedler,J., Carninci,P., Hayashizaki,Y. and Buerstedde,J.M.
Full-length cDNAs from bursal lymphocytes to facilitate gene
function analysis
Unpublished (2004)
JOURNAL Contact: Caldwell RB
COMMENT GSF - Forschungszentrum, Institut fuer Molekulare Strahlenbiologie
Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY.
FEATURES
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Location/Qualifiers
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/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="26j22e5"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/clone_lib="riken1"
/note="CB inbred strain"
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Query Match 2.3%; Score 84.2; DB 1; Length 727;
Best Local Similarity 47.2%; Pred. No. 6.9e-06;
Matches 297; Conservative 0; Mismatches 323; Indels 9; Gaps 1;
QY 1296 CTTGCGGCCCGCTGCTCTGGAGTTTGAACAGGAATTCAGATGCTGCTGGCTTCAT 1355
DB 720 GTGTCGGGCTGCGCATCTGTCAGTCCAGAGCGAGGAGCTCTCTGCACTGCTGGG 661
QY 1356 GACCTTCCTCAAGCAGTACGCGCCCGAGTTCGTGACCGGGTACACATCATCACTTGA 1415
DB 660 GGAGTTTGTGGCATTTGTGGACCCCGACGTCATCACGGGGTACAACTCCAGAACTTGA 601
QY 1416 CTGGCCCTTCCTCTGACCAAGCTGACGGAGATCTTACAAGGTCCCGCTCGACGGGTACGG 1475
DB 600 CTGCGCTTACCTATGACGCGCGGACGTGCTCAGGGTCTCGTCTTCCGTTCTTGGG 541
QY 1476 GCGATGAAACGCGCGGGGTGTGTTCCGCGTGTGGGACATCGGCCAGAGCCACTTTTCAGAA 1535
DB 540 CCGCATTCGGGGCGCGCGCTCGCAGCTCGCGGAGCGCTCTTCCAGTCCGCCAGTTGGG 481
QY 1536 GCGCAGCAAGATCAAGTGA-----ACGGATGTGTGAATCGACATGTACGGCAT 1586
DB 480 CCGCAGGAGACCAAAAGTGTGA CCGCTGAGGGGAGAGTCAACATTCAGACCTCTCTGAGGT 421
QY 1587 CATCACCCAGAGGTCAAACTCTCCAGCTCAAGCTGAACGCGCTCGCGGAGCGCGTCTT 1646
DB 420 GCTGTCGGGAGCACAACCTCGGCTCTCTATACCTCAATGGGTTCAGCGGCATTTCT 361
QY 1647 GAAGACAAAGAAAGAGTCTGAGTACCGGCAATCCCGCTACTACGCTCTCGGGCC 1706
DB 360 GCACGAGCAGAAAGGAGAGCTACCCCATAGCATCATCACCGACCTTACAGCAGGCTCGGA 301
QY 1707 CGCGCAGCGCGGGGTATCGCGAGTATTTGTGCAGGACTCGCTGCTGCTCGGCGAGCT 1766
DB 300 TCAGACGCGGCGCGCTTGGCGCTCTACTGCTGAAAGGACGAGTGTCTCGCGCTGCGGCT 241
QY 1767 GTTCTTCAAGTTTCTGCGGCACCTGGAGCTTTTCGCGCGTTCGCGGCGCTGGGGGATCAA 1826
DB 240 GTTGAGCGGCTGATGGTGTGGTGAACACAGTGGAGATGGCGCGCTCACCGGCGTCCC 181
QY 1827 CATCACCGCACCATCTACGACGGCCAGAGATCCGCGTCTTTCAGTGCCTCTCTGGCCT 1886
DB 180 TCTCGCTACTGCTGCGCGGGGACAGAGGTCAAGTGTGTGGCAGAGCTGCTCAGACA 121
QY 1887 TGGGGCCAGAGGGCTTCATCTCTGCGGG 1915
DB 120 GGCCATCGAGGAGATCTGCTGTGCGGG 92
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CG754548/c
LOCUS CG754548 1956 bp DNA linear GSS 24-OCT-2003
DEFINITION P50-1-All.za Ppa EcoRI BAC library Pristionchus pacificus genomic,
genomic survey sequence.
ACCESSION CG754548
VERSION CG754548.1 GI:37980151
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
REFERENCE 1 (bases 1 to 1956)
AUTHORS Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
pacificus
Mol. Genet. Genomics 269 (5), 715-722 (2003)
JOURNAL
MEDLINE 22835951
PUBMED 12884007
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
FEATURES
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Location/Qualifiers
1..1956
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/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."
ORIGIN
Query Match 2.2%; Score 82.2; DB 9; Length 1956;
Best Local Similarity 33.7%; Pred. No. 1.7e-05;
Matches 543; Conservative 0; Mismatches 1053; Indels 15; Gaps 3;
QY 1832 CCCCACCATCTACGACGGCCAGCAGATCCGCGTCTTTCAGTGCCTCTCTGCGCTTGGG 1891
DB 1713 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1654
QY 1892 GCCAAGAGGGCTTATCTCTGCGGACACCCAGGGGCGGTTTCGGGGGCTTCGACAAGGAGG 1951
DB 1653 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1594
QY 1952 CGCCCAAGCGCGCGCGCGTGTCTCGGGGGGAGGGGAGCGGCGCGGGGAGACGGGACCGGG 2011
DB 1593 GGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1534
QY 2012 ACAGAGGATAGAGCAGCAGCAGGAGCAGGAGCAGGGGACGAGCGAGAGGTTCGCGCGCG 2071
DB 1533 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1474
QY 2072 AGACCGGGGGGGCGGACAGCTTGGGTACGAGGGGGGGCGGGGTCTTCACACCCACCTCCGGGT 2131
DB 1473 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1414
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QY 2132 TTCACTGACCCCGTGTGTGTTTGAATTTTCCAGCCTGTACCCAGCATCATCCAGG 2191
Db 1413 GCCCGCGGCGCGCGCGG-----CCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1361
QY 2192 CCAACAACCTGTGCTTTCAGTACGCTCTCCCTGGGCGGAGGCGGTGCGCACTGTGAGG 2251
Db 1360 CCCCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGNG 1301
QY 2252 CGGACCGGACTTACCTGGAGATCGAGGTGGGGCGCGCGGTGTTTCTGTGAAGGCC 2311
Db 1300 C---CGGNGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1244
QY 2312 ACCTAGCGAGACCTGTCTGAGCATCTCTCTGCGGACTGGCTGGCATGCGAAAGCAGA 2371
Db 1243 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1184
QY 2372 TCGGCTCGGGATCCCCAGAGACCCCGAGAGCGCGCTCTCTCGACAAGCAACAGG 2431
Db 1183 GCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1124
QY 2432 CGCGCATCAAGTGTGTGCAACTCGGTGTAGGGTTTACCGGGGCGGACGCGTCTTC 2491
Db 1123 GNGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1064
QY 2492 TGCCCTGTGACGCTGGCGCGCACCGTGAACACCATCGCGCGCGGAGATGCTCTCGCGA 2551
Db 1063 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1004
QY 2552 CGCGCGGTGATGTGACGCGCGCGCTGGGCGGAGTTTGATGAGCTGTGCGCGACTTTCGG 2611
Db 1003 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 944
QY 2612 AGCGCGCGCATGCGCGCGCGCGCTCGTACTCTCATGGCATCATCTACGGGGACAGG 2671
Db 943 CNGNGNCCCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 884
QY 2672 ACTCCATTTTCTGTCGCGCGCGCTCACGCGCGCGCGCGCTGTGTGGCATGGCGACA 2731
Db 883 CNGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 824
QY 2732 AGATGGGAGGCACATCTCGCGCGCGCTGTTCTCCCGCGATCAAGCTCGAGTGGAAA 2791
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QY 2792 AAACGTTACCAAGTGTGTCTCATGCGCAAGAAAAGTACATCGGCGTCACTCGGGG 2851
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RESULT 14
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LOCUS
DEFINITION
BP096735 Chlamydomonas reinhardtii C9 various conditions
Chlamydomonas reinhardtii cDNA clone MXL063h11_r 5', mRNA sequence.
ACCESSION
BP096735
VERSION
BP096735.1 GI:49468874
KEYWORDS
EST.
SOURCE
Chlamydomonas reinhardtii
ORGANISM
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE
1 (bases 1 to 453)
AUTHORS
Asamizu,E., Nakamura,Y., Miura,K., Fukuzawa,H., Fujiwara,S.,
Hirono,M., Iwamoto,K., Matsuura,Y., Minagawa,J., Shimogawara,K.,
Takahashi,Y. and Tabata,S.
TITLE
Establishment of Publicly Available cDNA Material and Information
Resource of Chlamydomonas reinhardtii (Chlorophyta), to Facilitate
Gene Function Analysis
JOURNAL
Phycologia (2004) In press
COMMENT
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.

FEATURES
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/db_xref="taxon:3055"
/clone="MXL063h11_r"
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conditions"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was made from a mixture of cells
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ORIGIN
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Best Local Similarity 51.9%; Pred. No. 1.8e-05;
Matches 218; Conservative 0; Mismatches 190; Indels 12; Gaps 1;

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QY 2281 GGGGCGCGAGCGCTGTCTTCTGTGAAGCGCCACAGTACCGGAGAGCTCTGAGAGTCTCTG 2340
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RESULT 15

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CNS010EW 1009 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION BACN03P19 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1009)

Genoscope.

Direct Submission

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) -

http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre

d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector

pBelOBAC11.

Location/Qualifiers

1..1009

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/note="end : SP6"

ORIGIN

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Best Local Similarity 29.7%; Pred. No. 2.2e-05;
Matches 131; Conservative 112; Mismatches 198; Indels 0; Gaps 0;

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Result No.	Score	Query		DB	ID	Description
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2	3717	100.0	3717	19	US-10-692-556-1	Sequence 1, Appli
3	3696	99.4	3723	9	US-09-904-065-3	Sequence 3, Appli
4	3696	99.4	3723	19	US-10-692-556-3	Sequence 3, Appli
5	3693	99.4	154746	10	US-09-827-688-8	Sequence 8, Appli
6	3059.8	82.3	3708	9	US-09-904-065-5	Sequence 5, Appli
7	3059.8	82.3	3708	19	US-10-692-556-5	Sequence 5, Appli

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RESULT 2
US-10-692-556-1
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; Publication No. US20040115623A1
; GENERAL INFORMATION:
; APPLICANT: Home, Fred
; APPLICANT: Wathen, Michael
; APPLICANT: Hopkins, Todd
; APPLICANT: Thomsen, Darrell
; TITLE OF INVENTION: A Method for Treating Herpes Virus
; FILE REFERENCE: 00221
; CURRENT APPLICATION NUMBER: US/10/692,556
; CURRENT FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3717
; TYPE: DNA
; ORGANISM: herpes simplex
US-10-692-556-1

Query Match 100.0%; Score 3717; DB 19; Length 3717;
Best Local Similarity 100.0%; Pred. No. 0;
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Qy	541	ACCGTCATCAGCTTCTGGGTCTGACCCCGGAGGCTGATCGGCACCTCGAGTGCCGT	600
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Qy	601	GGCAGCGGAGTACTTTTACATGAACAAAGCGGAGGTGGATCGGCACCTCGAGTGCCGT	660
Db	601	GGCAGCGGAGTACTTTTACATGAACAAAGCGGAGGTGGATCGGCACCTCGAGTGCCGT	660
Qy	661	GCCCGCGCGATCTCTGAGCGCTGCGCGCGCTGCGCGAGTCTGCGGCGGCGTCTG	720
Db	661	GCCCGCGCGATCTCTGAGCGCTGCGCGCGCTGCGCGAGTCTGCGGCGGCGTCTG	720
Qy	721	TTCCGCGGATCTCCGCGGACACTTTCAGGCGGAGGTGGAGCGCGCGCGATCTAC	780
Db	721	TTCCGCGGATCTCCGCGGACACTTTCAGGCGGAGGTGGAGCGCGCGCGATCTAC	780
Qy	781	TATTACGAAACGCGCCGACCTGTACTACCGCGTCTTTCGTCGAAAGCGGCGCGCGTG	840
Db	781	TATTACGAAACGCGCCGACCTGTACTACCGCGTCTTTCGTCGAAAGCGGCGCGCGTG	840
Qy	841	GCCTACCTGTGCGAACTTTTTCGCGCGATCAGAAAGTACGAGGGGGCGTTCGAGCC	900
Db	841	GCCTACCTGTGCGAACTTTTTCGCGCGATCAGAAAGTACGAGGGGGCGTTCGAGCC	900
Qy	901	ACCACCGGTTTATCTGGAACAACCGGGGTTTGTACCTTCGCGTGTGATCGGCTCAAG	960
Db	901	ACCACCGGTTTATCTGGAACAACCGGGGTTTGTACCTTCGCGTGTGATCGGCTCAAG	960
Qy	961	CCCGCGCGGGAACCGCGCGCGCCCAACCGCGCGCGCGCGGCTTCGGAACCTCGAGC	1020
Db	961	CCCGCGCGGGAACCGCGCGCGCCCAACCGCGCGCGCGCGGCTTCGGAACCTCGAGC	1020
Qy	1021	GACGTGAGTTTAACTGCAACCGCGGCAAACTGCGCGTTCGAGGGGGCGTTCGAGCCTG	1080
Db	1021	GACGTGAGTTTAACTGCAACCGCGGCAAACTGCGCGTTCGAGGGGGCGTTCGAGCCTG	1080
Qy	1081	CCGCGCTACAAGCTCATGTCTTCGATATCGAATGCAAGGCGCGGGGGAGGAGGAGCTG	1140
Db	1081	CCGCGCTACAAGCTCATGTCTTCGATATCGAATGCAAGGCGCGGGGGAGGAGGAGCTG	1140
Qy	1141	GCCTTTCGCGTTCGCGGAAACCGCGGAGACCTCGTTCATCAGATCTCTGTCTGTCTAC	1200
Db	1141	GCCTTTCGCGTTCGCGGAAACCGCGGAGACCTCGTTCATCAGATCTCTGTCTGTCTAC	1200
Qy	1201	GACCTGTCACACCGCGCTTCGAGCAATCTCTCTGTGTTTTCGTCGATCTCTGAGACCTC	1260
Db	1201	GACCTGTCACACCGCGCTTCGAGCAATCTCTCTGTGTTTTCGTCGATCTCTGAGACCTC	1260
Qy	1261	CCGAGTCCCACTCAGCGATCTCGCTTCAGGGGCGTCCGCGCGCGCTCGTCTCTGAG	1320
Db	1261	CCGAGTCCCACTCAGCGATCTCGCTTCAGGGGCGTCCGCGCGCGCTCGTCTCTGAG	1320
Qy	1321	TTTGAACGAAATTCAGATGCTGTGCGCTTCATGACCTTCGTCGAGCAGTACGCGCCC	1380
Db	1321	TTTGAACGAAATTCAGATGCTGTGCGCTTCATGACCTTCGTCGAGCAGTACGCGCCC	1380
Qy	1381	GAGTTCTGACCGGGTACAACATCAATCACTTCGACTGCGCGCTTCGTCGACCAAGCTG	1440
Db	1381	GAGTTCTGACCGGGTACAACATCAATCACTTCGACTGCGCGCTTCGTCGACCAAGCTG	1440

Qy	1441	ACGAGATCTACAGGTCCCGCTCGAGGGGTACCGGGCGCATGAACGGCGGGGTGTGTTC	1500
Db	1441	ACGAGATCTACAGGTCCCGCTCGAGGGGTACCGGGCGCATGAACGGCGGGGTGTGTTC	1500
Qy	1501	CGCGTGTGGACATCGGCCAGAGCACCTTTTCAGAAAGCGCAGCAAGATCAAGGTGAACGG	1560
Db	1501	CGCGTGTGGACATCGGCCAGAGCACCTTTTCAGAAAGCGCAGCAAGATCAAGGTGAACGG	1560
Qy	1561	ATGTGAAATCGACATGTATCGGATCATCAACCGCAAGGTCAAACTCTCAGCTACAAAG	1620
Db	1561	ATGTGAAATCGACATGTATCGGATCATCAACCGCAAGGTCAAACTCTCAGCTACAAAG	1620
Qy	1621	CTGAACCGCGTCCGCGAGGCGCTTGAAGACAAAGAGGATCTGAGCTACCGCGAC	1680
Db	1621	CTGAACCGCGTCCGCGAGGCGCTTGAAGACAAAGAGGATCTGAGCTACCGCGAC	1680
Qy	1681	ATCCCGCGCTACTACGCTCTCGGGCGCGCAGCGCGGGGTGATCGGCGAGTATTTGTGTG	1740
Db	1681	ATCCCGCGCTACTACGCTCTCGGGCGCGCAGCGCGGGGTGATCGGCGAGTATTTGTGTG	1740
Qy	1741	CAGACTCGCTGTGCTGGCGAGCTGTTCTTCAAGTTTCTGCGCGACCTCGAGCTTTCC	1800
Db	1741	CAGACTCGCTGTGCTGGCGAGCTGTTCTTCAAGTTTCTGCGCGACCTCGAGCTTTCC	1800
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Db	1801	GCGGTCCGCGCTCGCGGGCATCAACATCAACCGCACCATCTACGCGCGCAGCAGATC	1860
Qy	1861	CGCGTCTTCAAGTCTCTGCGCTTTCGCGCGCAGAAAGGCTTTCATCTCTCGCGACACC	1920
Db	1861	CGCGTCTTCAAGTCTCTGCGCTTTCGCGCGCAGAAAGGCTTTCATCTCTCGCGACACC	1920
Qy	1921	CAGGGCGGTTTTCGCGCTTCGCAAGAGCGCGCCAAAGCGCGCGCTGCTCGGGGG	1980
Db	1921	CAGGGCGGTTTTCGCGCTTCGCAAGAGCGCGCCAAAGCGCGCGCTGCTCGGGGG	1980
Qy	1981	GAGGGAGCGCGCGGGGACGGGAAACGGGACAGGATAGAGACGACGAGCAGCAG	2040
Db	1981	GAGGGAGCGCGCGGGGACGGGAAACGGGACAGGATAGAGACGACGAGCAGCAG	2040
Qy	2041	GACGGGACGAGCGCGAGAGTTCGCGCGAGACCGGGGGCGCGACGTTGGGTACCAAG	2100
Db	2041	GACGGGACGAGCGCGAGAGTTCGCGCGAGACCGGGGGCGCGACGTTGGGTACCAAG	2100
Qy	2101	GGGGCGCGGTCTCGAGACCCCACTTCGCGGTTTTCAGCTCGACCGCGTGGTGTTCAC	2160
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Qy	2221	CTGCGGCGAGGCGCTCGGCACTCTGAGGGCGAGCCGGGACTACCTGGAGATCGAGGTG	2280
Db	2221	CTGCGGCGAGGCGCTCGGCACTCTGAGGGCGAGCCGGGACTACCTGGAGATCGAGGTG	2280
Qy	2281	GGGGCGGACGGCTGTTCTGTAAGCCCACTTCGCGAGAGCTGCTGAGGATCTCTG	2340
Db	2281	GGGGCGGACGGCTGTTCTGTAAGCCCACTTCGCGAGAGCTGCTGAGGATCTCTG	2340
Qy	2341	CTGCGGACTGCTGGGCGCATCGGATCCGCTCGCGGATCCCCCAGAGCACCCCC	2400
Db	2341	CTGCGGACTGCTGGGCGCATCGGATCCGCTCGCGGATCCCCCAGAGCACCCCC	2400
Qy	2401	GAGGAGCGCTCTCTCGACAAGCAACAGCGCGCATCAAGGTGGTGTGCAATCGGTG	2460
Db	2401	GAGGAGCGCTCTCTCTCGACAAGCAACAGCGCGCATCAAGGTGGTGTGCAATCGGTG	2460
Qy	2461	TACGGTTTCAACGGGGCGCAGCAGCTTCTGCGCTTCGCTGCGCGCGCGCACCGGTG	2520
Db	2461	TACGGTTTCAACGGGGCGCAGCAGCTTCTGCGCTTCGCTGCGCGCGCGCACCGGTG	2520
Qy	2521	ACGACCATCGGCGCGAGATGCTCTCTCGCGAGCGCGCGTACGTGCAACGCGCTGGGCG	2580

Db 2521 ||||| AGACATCGCGCGAGATGCTCTCGGACCGCGCGTACGTGACGCGGCGCTGGCG 2580
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Db 2641 TACTCCATCGCATCATCTACGGGACACGGACTCCATTTTGTGTCGCGGCGCTC 2700
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RESULT 3
US-09-904-065-3
; Sequence 3, Application US/09904065
; Patent No. US20020076789A1
; GENERAL INFORMATION:
; APPLICANT: Homa, Fred
; APPLICANT: Wathen, Michael
; APPLICANT: Hopkins, Todd
; APPLICANT: Thomsen, Darrell
; TITLE OF INVENTION: A Method for Treating Herpes Virus
; FILE REFERENCE: 00221
; CURRENT APPLICATION NUMBER: US/09/904,065
; CURRENT FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 3723
; TYPE: DNA
; ORGANISM: herpes simplex
US-09-904-065-3
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Best Local Similarity 99.8%; Pred. No. 0;
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QY 3655 GCGGCGGTACGGCGGAGAACTCGTGAATGTTGCATAGAGCTTTGATCTAGCA 3714
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QY 3715 TGA 3717
Db 3721 TGA 3723
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RESULT 4

US-10-692-556-3
; Sequence 3, Application US/10692556
; Publication NO. US20040115623A1
; GENERAL INFORMATION:
; APPLICANT: Homa, Fred
; APPLICANT: Wathen, Michael

; APPLICANT: Hopkins, Todd
; APPLICANT: Thomsen, Darrell
; TITLE OF INVENTION: A Method for Treating Herpes Virus
; FILE REFERENCE: 00221
; CURRENT APPLICATION NUMBER: US/10/692,556
; CURRENT FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 3723
; TYPE: DNA
; ORGANISM: herpes simplex
US-10-692-556-3

Query Match 99.4%; Score 3696.2; DB 19; Length 3723;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3714; Conservative 0; Mismatches 3; Indels 6; Gaps 1;
QY 1 ATGTTTGTGCGCGGGCGGCCGACTTCCCGCGGGGGAAGTCCGGCGGCTCGGGCGGCG 60
Db 1 ATGTTTGTGCGCGGGCGGCCGCGCTTCCCGCGGGGGAAGTCCGGCGGCTCGGGCGGCG 60
QY 61 TCTGGTTTTTGGCCCCCAACACCCCGGGGAGCCACCCAGACGGCACCGCGCGCTTGC 120
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QY 121 CGCGGAGAACTTCTACAACCCCGACCTCGCTCAGACCGGAAACGAGCAAAAGGCCCC 180
Db 121 CGCGGAGAACTTCTACAACCCCGACCTCGCTCAGACCGGAAACGAGCAAAAGGCCCC 180
QY 181 GGGCGGCTCAGCGCATACGTACTACAGCAGTGCAGAAATTTTCGATTTATCGCCCG 240
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Db 301 CGGCGCGCCCTAAGGTGTACTGCGGGGGGAGCAGCGCGCGCTCTCCGCTGGGCGCG 360
QY 361 GAGGCTTCTGGCGCGCTCGCTTGGCGCTGTGGGCGGTGGCGACCATGCCCGCCAGGGG 420
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QY 421 TTCGACCCACCGTCAACCGTCTTCCACGTGTACGACATCTGGAGACGCTGGAACACGCG 480
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Db 541 ACCGTATCAGCTTCTGGGTCTGACCCCGGAAAGGCCATCGCGTCCCGTTCACGCTTAC 600
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Db 781 TATTACGAAACGCGCCGACCTGTACTACCGCGCTTTCGTGCGAAGCGGGCGCGCTG 840

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Qy 3715 TGA 3717
Db 3721 TGA 3723
RESULT 5
US-09-827-688-8
; Sequence 8, Application US/09827688
; Publication No. US20030165476A1
; GENERAL INFORMATION:
; APPLICANT: ORSON, FRANK
; APPLICANT: KINSEY, BERMA
; APPLICANT: BHOGAL, BALBIR
; TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: P01949US1/10004014
; CURRENT APPLICATION NUMBER: US/09/827,688
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,680
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 154746
; TYPE: DNA
; ORGANISM: HERPESVIRUS 2

US-09-827-688-8
Query Match 99.4%; Score 3693; DB 10; Length 154746;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3712; Conservative 0; Mismatches 5; Indels 6; Gaps 1;
Qy 1 ATGTTTGTGCGGGCGGCGCGGCTTCCCGCGGGGAGTTCGGCGGCTTCGGCGGCG 60
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Db 63505 GGTTCGTGAGAGAGCGCGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGCGCTC 63564
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Qy 421 TTCGACCCACCGTCAACCGTCTTCAACGATGACGATCTGAGAGCATGAGGAGCATGGA 480
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Qy 961 CCCGCGCGGAGACGCGCGCGGCGCAACCGCGCGCGCGCGCGCGCTTCGGAACCTTCGAGC 1020
Db 64225 CCCGCGCGGAGACGCGCGCGGCGCAACCGCGCGCGCGCGCGCGCTTCGGAACCTTCGAGC 64284

QY	1021	GACGTCGAGTTTAACTGCA CGCGCGA CAACTTGGCCGTCGAGGGGGCCCATGTGTGACCTG	1080
Db	64285	GACGTCGAGTTTAACTGCA CGCGCGA CAACTTGGCCGTCGAGGGGGCCCATGTGTGACCTG	64344
QY	1081	CGGCGCTACAAGCTCATGTCTTCGATATCGAATCGAAGGCGGGGGGAGGACGAGCTG	1140
Db	64345	CGGCGCTACAAGCTCATGTCTTCGATATCGAATCGAAGGCGGGGGGAGGACGAGCTG	64404
QY	1141	GCCTTTCGGGTGCGGGAAGCGCCGGAAGACCTCGTCAATCCAGATCTCTGTCTGTCTTAC	1200
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QY	1201	GACCTGTCCACACCGCCCTCGAGACATCTCTCTGTGTTTTCGTCGATCTCGGACCTC	1260
Db	64465	GACCTGTCCACACCGCCCTCGAGACATCTCTCTGTGTTTTCGTCGATCTCGGACCTC	64524
QY	1261	CCCGAGTCCCACTCAGCGATCTGCGCTCCAGGGGCGTCCGGCCCGCCGTCCTGTGAG	1320
Db	64525	CCCGAGTCCCACTCAGCGATCTGCGCTCCAGGGGCGTCCGGCCCGCCGTCCTGTGAG	64584
QY	1321	TTTGACGCGAATTCGAGATGCTGCTGGCCTTCATGACCTTCGTCAAGCAGTACGGCCCC	1380
Db	64585	TTTGACGCGAATTCGAGATGCTGCTGGCCTTCATGACCTTCGTCAAGCAGTACGGCCCC	64644
QY	1381	GAGTTCGTGACGGGTACAACATCATCAATCAATCAATCAATCAATCAATCAATCAATCA	1440
Db	64645	GAGTTCGTGACGGGTACAACATCATCAATCAATCAATCAATCAATCAATCAATCAATCA	64704
QY	1441	ACGAGATCTACAAGTCCCGCTCGACGGGTACGGGCGCATGAACGGCGGGGTGTGTC	1500
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Db	64765	CGCGTGTGGGACATCGGCAGAGCCATTTTCAGAAAGCGCAGCAAGATCAAGGTGAACGGG	64824
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Db	64825	ATGTGTGAATCGCATGATGCGCATCATCAACGCAAGAGTCAACTCTCAGCTACAG	64884
QY	1621	CTGAACCGCGCTCGCGAGCGCTCTTGAAGACAAAGAAAGGATCTGAGCTACCGGAC	1680
Db	64885	CTGAACCGCGCTCGCGAGCGCTCTTGAAGACAAAGAAAGGATCTGAGCTACCGGAC	64944
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QY	1741	CAGGACTCGCTGCTGGTGGGAGCTGTCTTCAAGTTTCTGCCGACCTGGAGCTTTCC	1800
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Db	65065	CGCGTCGCGCGCTGGCGGCGATCAATCAACCGCACCATCTACGACGGCCAGCAGATC	65124
QY	1861	CGCGTCTTACGTCCTCTCGCTTCGCGGCGCAGAAAGGCTTCATCTCTCCCGGACACC	1920
Db	65125	CGCGTCTTACGTCCTCTCGCTTCGCGGCGCAGAAAGGCTTCATCTCTCCCGGACACC	65184
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Db	65185	CAGGGCGGTTTCGGGGCTTCGACAGAGAGCGCCCAAGCGCCCGCGCTGCTCGGGG	65244
QY	1981	GAAGGGGAGCGCGGGGAGCGGAAACGGGACAGAGATAAGGACGACGACGA-----G	2034
Db	65245	GAAGGGGAGCGCGGGGAGCGGAAACGGGACAGAGATAAGGACGACGACGACGAGCGGG	65304
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Db	65305	GACGAGGACGGGACGACGCGGAGAGGTTCGCGCGAGACCGGGGGCCCGACGTTGGG	65364
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QY	2215	CTCTCCCTCGCGGCCGAGGCGCTCGCACCTGAGAGCGGACCGGGACCTACTCGAGATC	2274
Db	65485	CTCTCCCTCGCGGCCGAGGCGCTCGCACCTGAGAGCGGACCGGGACCTACTCGAGATC	65544
QY	2275	GAGTGGGGGGCCGACCGGCTGTCTTCTGTGAAGCCCACTGACCGGAGAGCTGCTGAGC	2334
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QY	2335	ATCTCTGTGCGGACTGCGCTGGCCCATCGAAAGCAGATCGCGCTCGCGATCCCCCAGAGC	2394
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QY	2455	TCGCTGTACGGGTTTCAACGGGGCGCAGACGGTCTTCTGCGCTGCTGCGAGTGGCGGCC	2514
Db	65725	TCGCTGTGTACGGGTTTCAACGGGGGTGACACGGTCTTCTGCGCTGCTGCGAGTGGCGGCC	65784
QY	2515	ACCGTGAACGACATCGCGCGGAGATGCTCTCGACAGCGCGCGGTAGTGCACGCGGCG	2574
Db	65785	ACCGTGAACGACATCGCGCGGAGATGCTCTCGACAGCGCGCGGTAGTGCACGCGGCG	65844
QY	2575	TGGCGGAGTTTCGATGAGCTGCTGGCGGACTTTTCGAGAGGCGCGCGCATGCGCGCCCC	2634
Db	65845	TGGCGGAGTTTCGATGAGCTGCTGGCGGACTTTTCGAGAGGCGCGCGCATGCGCGCCCC	65904
QY	2635	GGTCCGTACTCTACGCGCATCTACGGGACAGGACCTCCATTTTCTGTTTGTGCGCG	2694
Db	65905	GGTCCGTACTCTACGCGCATCTACGGGACAGGACCTCCATTTTCTGTTTGTGCGCG	65964
QY	2695	GGCTCTACGGCGCGCGCTGTTGGCCATGGGCGCAAGATGGCGAGCCACATCTCGCGC	2754
Db	65965	GGCTCTACGGCGCGCGCTGTTGGCCATGGGCGCAAGATGGCGAGCCACATCTCGCGC	66024
QY	2755	GCGTGTTCCTCCCGCATCAAGCTCGAGTGCAGAAAGAAAGGTTTCAAGAGCTGCTGCTC	2814
Db	66025	GCGTGTTCCTCCCGCATCAAGCTCGAGTGCAGAAAGAAAGGTTTCAAGAGCTGCTGCTC	66084
QY	2815	ATCGCCAAGAAAAGTACATCGGCGTCACTCGCGGGGCAAGATGCTCATCAAGGGCGTG	2874
Db	66085	ATCGCCAAGAAAAGTACATCGGCGTCACTCGCGGGGCAAGATGCTCATCAAGGGCGTG	66144
QY	2875	GATCTGTGGCGCAAAAAAACAATGCGCGTTCATCAACCGCACCTCCAGGGCCCTGCTCGAC	2934
Db	66145	GATCTGTGGCGCAAAAAAACAATGCGCGTTCATCAACCGCACCTCCAGGGCCCTGCTCGAC	66204
QY	2935	CTGTGTTTTCAGCAGATACCGTATCCGAGCGCGCCCGCGGTTTACGAGGCGCCCGCA	2994
Db	66205	CTGTGTTTTCAGCAGATACCGTATCCGAGCGCGCCCGCGGTTTACGAGGCGCCCGCA	66264
QY	2995	GAGGAGTGGTGGCGGACCCCTGCGCGAGGAGCTGAGGGGCTGCGGGCGCTCTCGTA	3054
Db	66265	GAGGAGTGGTGGCGGACCCCTGCGCGAGGAGCTGAGGGGCTGCGGGCGCTCTCGTA	66324
QY	3055	GACGCCCATCGGCGCATCAACCGACCGGAGAGGAGCATCCAGGACTTTTGTCTCACCGGCC	3114
Db	66325	GACGCCCATCGGCGCATCAACCGACCGGAGAGGAGCATCCAGGACTTTTGTCTCACCGGCC	66384
QY	3115	GAACTGAGGACACCCGCGCGGTACACCAAGCGCTGTGCCCCACCTGACGGTGTAT	3174
Db	66385	GAACTGAGGACACCCGCGCGGTACACCAAGCGCTGTGCCCCACCTGACGGTGTAT	66444
QY	3175	TACAGCTCATGGGCCCGCGCGCAGGTCCCGTCCATCAAGGACCGGATCCCGTACGTG	3234


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Db 66445 TACAAGCTCATGCCCGCGCGAGTCCCGTCCATCAAGGACCGGATCCCGTACGTG 66504
Qy 3235 ATCGTGGCCAGACCGCGAGGTAGAGGAGCGGTCCGCGGCTGGCGCCCTCCCGGAG 3294
Db 66505 ATCGTGGCCAGACCGCGAGGTAGAGGAGCGGTCCGCGGCTGGCGCCCTCCCGGAG 66564
Qy 3295 CTAGAGCGCCCGCGCCCGCACGGGACAGAGCCCGCGCCCGCCAGCGGCGCTGCGCTCCCGGCG 3354
Db 66565 CTAGAGCGCCCGCGCCCGCACGGGACAGAGCCCGCGCCCGCCAGCGGCGCTGCGCTCCCGGCG 66624
Qy 3355 AAGCGCCCGCGGAGAGCGCGCTCGCATGCGACCGCCCGCGGAGCGCGCTGCAAGCGCCCGC 3414
Db 66625 AAGCGCCCGCGGAGAGCGCGCTCGCATGCGACCGCCCGCGGAGCGCGCTGCAAGCGCCCGC 66684
Qy 3415 AAGCTGCTGGTTCGCGAGCTGCGGAGGATCCCGGATCGCGGATCGCGGCGGCGTTCG 3474
Db 66685 AAGCTGCTGGTTCGCGAGCTGCGGAGGATCCCGGATCGCGGATCGCGGCGGCGTTCG 66744
Qy 3475 CTCAACACGAGCTATTACTTCTCGCACCTGCTGGGCGCGCTGCGTGACGTTCAAGGCC 3534
Db 66745 CTCAACACGAGCTATTACTTCTCGCACCTGCTGGGCGCGCTGCGTGACGTTCAAGGCC 66804
Qy 3535 CTGTTTGGAAATAACGCCAAGATCACCGAGAGTCTGTTAAAGAGGTTTAAATCCCGAGAG 3594
Db 66805 CTGTTTGGAAATAACGCCAAGATCACCGAGAGTCTGTTAAAGAGGTTTAAATCCCGAGAG 66864
Qy 3595 TGGCACCCCGGAGAGCGGTGCGCGCGCTCAGGCGCGGGGTTGGGCGCGCGGG 3654
Db 66865 TGGCACCCCGGAGAGCGGTGCGCGCGCTCAGGCGCGGGGTTGGGCGCGCGGG 66924
Qy 3655 GCCGCGCTACCGCGGAGGAAACTCGTCAATGTTGCATAGAGCCTTTGATCTCTAGCA 3714
Db 66925 GCCGCGCTACCGCGGAGGAAACTCGTCAATGTTGCATAGAGCCTTTGATCTCTAGCA 66984
Qy 3715 TGA 3717
Db 66985 TGA 66987
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RESULT 6

US-09-904-065-5

; Sequence 5, Application US/09904065

; Patent No. US20020076789A1

; GENERAL INFORMATION:

; APPLICANT: Homa, Fred

; APPLICANT: Mathen, Michael

; APPLICANT: Hopkins, Todd

; APPLICANT: Thomsen, Darrell

; TITLE OF INVENTION: A Method for Treating Herpes Virus

; FILE REFERENCE: 00221

; CURRENT APPLICATION NUMBER: US/09/904,065

; CURRENT FILING DATE: 2001-07-12

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5

; LENGTH: 3708

; TYPE: DNA

; ORGANISM: herpes simplex

US-09-904-065-5

Query Match 82.3%; Score 3059.8; DB 9; Length 3708;

Best Local Similarity 89.3%; Pred No. 0;

Matches 3321; Conservative 0; Mismatches 387; Indels 9; Gaps 2;

Qy 1 ATGTTTGTGCGCGCGCGCGCGCTTCCCGCGGGGAACTCGCGCGCTCGCGCGG 60

Db 1 ATGTTTGTGCGCGCGCGCGCGCTTCCCGCGGGGAACTCGCGCGCGCGCGG 60

Qy 61 TGTGGTGTGTTTGGTCCCGCCACAAACCGCGGGAGCCACCGAGCGACCGCGCTTGC 120

Db 61 TCCGGGTGTTTGGCGCGCGCGCGCGCTTCCCGGAGCGCGCC---GGGAGACCCCGCTTGT 117

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Qy 121 CGCGCGCAGAACTTCTCAAAACCCACCTCGCTCAGACCGGAACGAGCAAGGCGCC 180
Db 118 TTGAGGCAAAACTTTTACAACCCCTACCTCGCCCCAGTCGGGACGCAACAGAAAGCG 177
Qy 181 GGGCGGCTCAGCGCCATACGTACTACAGCGAGTGGAGCAATTTTCGATTTATCGCCCG 240
Db 178 GGGCAAAACCCAGCGCATACGTACTATAGCGAATCGATGAATTTTCGATTTATCGCCCG 237
Qy 241 GGTTCGCTGGAGAGAGCGCCCGCGGAGAGCGCACCGGGGTCCAGAGCGCGCTC 300
Db 238 CGGTGCTGGAGAGAGTGCCTCCCGGAGAAAGCGCGCGGGTGCACAGCGTCACTC 297
Qy 301 CGCGCGCGCTTAAGGTGCTACTGCGGGGGGAGAGCGCGAGTCTCTCGCGTGGGCGCG 360
Db 298 AAGCGCGCGCTCAAGGTGCTACTGCGGGGGGAGAGCGCGAGTCTCTCGCGTGGGTCG 357
Qy 361 GAGGCTTCTGGCGCGCTGCTGCGCTGCGGGGGTGGCGGACCATGCCCCCAAGGGG 420
Db 358 GCGCGCTTCTGGCGCGCGCTGCGCGCTGCGGGCGCGTGGAGCCACCGCGCGCGG 417
Qy 421 TTTGAGACCCACCGTCAACCGTCTTCCACGTGTACGACATCTCTGAGCACCGTGAACAC 480
Db 418 TTCAACCCACCGTCAACCGTCTTCCACGTGTACGACATCTCTGAGAACCGTGGAGCAC 477
Qy 481 TACAGCATGCGCGCGCGCTCCACGAGCGGATTTATGAGCGCCATCAACGCGCGCGG 540
Db 478 TAGCGCATGCGCGCGCGCTCCACGCGCGGTTTATGAGCGCCATCAACGCGCGG 537
Qy 541 ACCGTATCAGCTTCTGGGCTGACCCCGAGAGCGCATTCGGCTCGCGTTCACGCTAC 600
Db 538 ACCGTATCAGCTTCTGGGCTGACTCCGGAAGCGCACCGGCTGGCGCTTCACTGCTTAC 597
Qy 601 GGCACGCGCAGTACTTTTACATGAACAAGCGGAGGTGGATCGGCACCTCGAGTGCCT 660
Db 598 GGCACGCGCAGTACTTTTACATGAACAAGGAGGAGTTGACAGGACCCCTCAATGCC 657
Qy 661 GCCCGCGCGATCTCTGCGAGCGCTGCGCGCGCGCTGCGCGAGTTCGCGCGGGCGT 720
Db 658 GCCCACGAGATCTCTGCGAGCGCATGCGCGCGCGCTGCGCGAGTCCCCGGGCGGTCG 717
Qy 721 TTTCCGCGCATCTCCGCGGACCATTTTCGAGGCGGAGTGGTGGAGCGCGCGCGCTGAT 780
Db 718 TTTCCGCGCATCTCCGCGGACCATTTTCGAGGCGGAGTGGTGGAGCGCGCACCGACGT 777
Qy 781 TATTACGAAGCGCGCGCGCTGCTACTACCGCGCTTTCTGTCGGAAGCGGGCGCGCTG 840
Db 778 TACTACGAGAGCGCGCGCGCTGCTTTTACCGCGCTTCTACGTCGGAAGCGGGCGGTCG 837
Qy 841 GCCTACCTGTGCGACAACTTTTTCGCCCGCATCAGAGAAAGTACGAGGGGGCGCTCG 900
Db 838 TCGTACCTGTGCGACAACTTTTCGCCCGCATCAGAGAAAGTACGAGGGTGGGTCGAGCG 897
Qy 901 ACCACCGGTTTATCTCGGACAAACCGGGGTTTTCACCTTCGGCTGGTACCGCTCAAG 960
Db 898 ACCACCGGTTTATCTCGGACAAACCGGGGTTTTCGTCACCTTCGGCTGGTACCGCTCA 957
Qy 961 CCCGCGCGGGAACCGCGCGCGCCCAACCGCGCGCGCGCGCGCTTCGGAACCTCGAGC 1020
Db 958 CCGGGCCGGAACCAACACCTAGCCAGCGCGGGCGCGGATGGCTTCGGGACATCCAGC 1017
Qy 1021 GACGTGAGTTTAACTGCACGCGGACAACTTGGCGCGTTCGAGGGGGCGCATGTGTGAC 1080
Db 1018 GACGTGAGTTTAACTGTACGGGAGCAAACTTGGCCATTCGAGGGGGCGCATGAGCGAC 1077
Qy 1081 CCGGCTTCAAGCTCATGTGTTTCGATATCGAATCGAAGCGCGGGGGAGAGCAGCTG 1140
Db 1078 CCGGCTTCAAGCTCATGTGTTTCGATATCGAATCGAAGCGCGGGGGAGAGCAGCTG 1137
Qy 1141 GCCTTTCGGTTCGGGAACCGCGGACCTCGTCATCCAGATCTCTGCTGCTCTAC 1200
Db 1138 GCCTTTCGGTTCGGGAGACCGCGGAGACCTGGTATTCAGATATCTCTGCTCTAC 1197
Qy 1201 GACCTGTCCACCGCGCTCGAGCACATCTCTCTGTTTTCGCTCGGATCCTCGACCTC 1260
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Db 1198 |||||GACCTGTCCACGACCGCCCTGGAGCAGCTCTCTCTGTTTTCGCTCGGTCTCTGCACTC 1257
Qy 1261 CCGAGTCCCACTCAGCGATCTCGCTCCAGGGGCTCGCGGCCCTCGTCTCTGGAG 1320
Db 1258 CCGGAATCCCACTGAACGAGCTGGCGGCGAGGGGCTCGCCACGCGCGTGTCTGGAA 1317
Qy 1321 TTGACAGGAAATTCGAGATGCTGTGCTTATGACCTTCGTCAAGCAGTACGGCCCC 1380
Db 1318 TTGACAGGAAATTCGAGATGCTGTGCTTTCATGACCTTGTGAACAGTACGGCCCC 1377
Qy 1381 GAGTTCGTGACCGGTACAAATCATCAACTTCGACTGCGCTTCGTCTCGACCAAGCTG 1440
Db 1378 GAGTTCGTGACCGGTACAAATCATCAACTTCGACTGCGCTTCGTCTCGACCAAGTGT 1437
Qy 1441 ACGGAGATCTCAAGGTCCCGCTCGACGGGTACGGGGCATGAACGGCGGGGTGTGTTTC 1500
Db 1438 ACGGACATTTACAAGTCCCTCGACGGGTAGGCGCGCATGAACGGCGGGGCTGTTT 1497
Qy 1501 CGCTGTGGGACATCGGCAGAGCCACTTTAGAAAGCGCAGCAGATCAAGGTGAACGG 1560
Db 1498 CGCTGTGGGACATAGGCGAGAGCCACTTCAGAAAGCGCAGCAGATGAAGGTGAACGGC 1557
Qy 1561 ATGTTGAACATCGCATGTACGGCATCATCAACGACAAAGGTCAAACTCTTCAGCTTACAAG 1620
Db 1558 ATGTTGAACATCGCATGTACGGCATCATCAACGACAAAGATCAAGCTCTCGACTACAAG 1617
Qy 1621 CTGAACCGCGTGGCGAGCGCTCTTGAAGACAAAGAAAGGATCTGAGCTACCGGAC 1680
Db 1618 CTCAACCGGTGGCGAAGCGCTCTGAAGACAAAGAAAGGACCTGAGCTATCGGAC 1677
Qy 1681 ATCCCGCTACTAGCCTCGGGCCCGCGCAGCGCGGGGTGATCGGCGATTTGTGTG 1740
Db 1678 ATCCCGCTACTAGCCTCGGGCCCGCGCAACGCGGGGTGATCGGCGATCTGCATA 1737
Qy 1741 CAGGACTCGCTGCTGGTGGCGAGCTGTTCTTCAAGTTTCTGCGCACCTCGAGCTTTCC 1800
Db 1738 CAGGATTCCTGCTGCTGGTGGCGAGCTGTTTAAAGTTTGGCCCATCTGGAGCTCTCG 1797
Qy 1801 GCCGTGCGCGCTGGCGGGGATCAACATCACCGCACCATCTACGACGGCCAGAGATC 1860
Db 1798 GCCGTGCGCGCTGGCGGGTATTAAATCATCACCGCACCATCTACGACGGCCAGAGATC 1857
Qy 1861 CGCTCTTCAGTGCCTCGCTCGCTCGGGCCGAGAGGGCTTCATCTCGCGGACACC 1920
Db 1858 CGCTCTTCAGTGCCTCGCTCGCTCGGGCCGAGAGGGCTTATTCTCGCGGACACC 1917
Qy 1921 CAGGGCGGTTTCGGGGCTTCGACAAAGGAGGCGGCCAAAGCGCCGGCGCTGCTCGGGG 1980
Db 1918 CAGGGCGATTTAGGGGCGCCGGGGGAGGGGCCCAAGCGTCCGGCCGACGCCGGAG 1977
Qy 1981 GAAGGGAGCGCGCGGGGACGGGAAACGGGACGAGGATTAAGACGACGACGAGAGAG 2040
Db 1978 GACGAGGAGCGCGGAGGAGGGGGAGACG-----AGGACGAACGGAGAGGGC 2031
Qy 2041 GACGGGACGAGCGGAGAGGTCCGCGCGCAGACCGGGGCGCGCAGTGGGTACCGAG 2100
Db 2032 GGGGCGAGCGGGAGCCGAGGGGCGCGGGAGACCGCGCGCGGACGTTGGGGTACCGAG 2091
Qy 2101 GGGGCGCGGGTCTTCGACCCACCTTCGCGGTTCACGTTCGACCCCGTGGTGTGTTGAC 2160
Db 2092 GGGGCGAGGTCCTTGACCCCACTTCGCGGTTTCAGGTGAACCCCGTGGTGTGTTGAC 2151
Qy 2161 TTGTCAGCTGTATCCCGAGCATCATCCAGGCCCAAACTGTGCTTCAGTACGCTTCC 2220
Db 2152 TTGTCAGCTGTATCCCGAGCATCATCCAGGCCCAAACTGTGCTTCAGCACGCTTCC 2211
Qy 2221 CTGGGGCCGAGGCGCTCGCACCTGAGGCGGACCGGGACTACCTGGAGATCGAGTG 2280
Db 2212 CTGAGGGCCGACGCTGGCGACCTGGAGGGGGGAAGGACTACCTGGAGATCGAGTG 2271
Qy 2281 GGGGCGCAGCGCTGTCTTCGTGAAGGCCCACTGTAACGAGAGCTGCTGAGCATCTG 2340

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Db 2332 CTGCGGACTGGCTGGCCATGCGAAAGCAGATTCGCTCGCGGATTTCCCAAGAGAGCCCC 2391
Qy 2401 GAGGAGCGCTTCCTTCGACAAAGCAACAGCCGCCCATCAAGGTGCTGTAACCTCGGTG 2460
Db 2392 GAGGAGCGCTTCCTTCGACAAAGCAGAGAGCCGCCCATCAAGGTGCTGTAACCTCGGTG 2451
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Db 2512 ACGACCATCGGCGCGAGATGCTCTCGGAGCGCGGCCGATGCGCGGCCCGGGGCC 2571
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Qy 2641 TACTCCATGCGCATCATCTACGGGACACGAGCTCCATTTTTCGTTTGTGCGCGGCTC 2700
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Qy 2761 TTCTCTCCCGCATCAAGCTCGAGTGGGAAAAACGTTTCAACAGCTGCTCTCATCGCC 2820
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Db 2812 AAGAAAAAGTACATCGCGCTCATCTACGGGGTAAAGTGTCTCATCAAGGGCGTGGATCTG 2871
Qy 2881 GTGCGGAAAAAACAATCGGGGTTTATCAACGCACTCTCAGGGGCTGTGCTGACTGCTG 2940
Db 2872 GTGCGGAAAAAACAATCGGGGTTTATCAACGCACTCTCAGGGGCTGTGCTGACTGCTG 2931
Qy 2941 TTTTACGAGATACCGTATCCGAGCGCGCGCTTAGCGAGCGGCCCGCAGAGAGAG 3000
Db 2932 TTTTACGAGATACCGTATCCGAGCGCGCGCGCTTAGCGAGCGGCCCGCAGAGAGAG 2991
Qy 3001 TGGCTGCGCGACCCCTCGCCCGAGGAGCTGCAAGCGCTTCGAGGGCGCTCTCTGTAAGCGCC 3060
Db 2992 TGGCTGCGCGACCCCTCGCCCGAGGAGCTGCAAGCGCTTCGAGGGCGCTCTCTGTAAGCGCC 3051
Qy 3061 CATCGGCGATACCGACCCGAGAGAGGACATCCAGGACTTTGTCTTCACCGCGGAAGCTG 3120
Db 3052 CATCGGCGATACCGACCCGAGAGGAGACATCCAGGACTTTGTCTCTCACCGCGGAAGCTG 3111
Qy 3121 AGCAGACACCCGCGCGGTACACCAACAGCGCTGCGCCACCTGAGCGGTGATTACAAG 3180
Db 3112 AGCAGACACCCGCGCGGTACACCAACAGCGCTGCGCCACCTGAGCGGTGATTACAAG 3171
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Db 3172 CTGATGGCCCGCGCGCAGGTCCTGATCAAGGACCGGATCCCGTACGTGATCGTG 3231
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Db 3292 GCCCGCGCCCGAGGGGACGAGCCCGCCCGCGGGCTTGCCTCTCCCGCGCAAGGCGC 3351
Qy 3361 CCCCGGAGAGCGCTGCGCATGCGACCCCGCGGAGCGGCTCAAGAGCCCGCGCAAGCTG 3420
Db 3352 CCCCGGAGAGCGCTGCGCATGCGACCCCGCGGAGCGGCTCCCAAGCCCGCGCAAGCTG 3411

QY 3421 CTGGTCTCCGAGCTGCGGAGATCCCGGTACGCCATCGCCGGGGCGTTCCGCTCAAC 3480
DB 3412 CTGGTCTCCGAGCTGCGCCGAGATCCCGCATACGCCATTTGCCACGCGCTCGCCCTGAAC 3471
QY 3481 ACGGACTATTACTTCTCGACCTGCTGGGGGGCGCTCGTGACGTTCAAGGCCCTGTTT 3540
DB 3472 ACGGACTATTACTTCTCCACCTGTTGGGGGGCGGTGCGTGACATTTCAAGGCCCTGTTT 3531
QY 3541 GGAAATAACGCCAAGATCAACGAGAGTCTGTTAAAGAGGTTTATTCGCCGAGAGCTGGCAC 3600
DB 3532 GGGATAACGCCAAGATCAACGAGAGTCTGTTAAAGAGGTTTATTCGCCGAGAGTGGCAC 3591
QY 3601 CCCCCGACGAGCTGCGCCGCGGCTCAGGGCCGCGGGTTTCGGGCGCGCGGGGGCGCGC 3660
DB 3592 CCCCCGACGAGCTGCGCCGCGGCTCAGGGCCGCGAGGTTTCGGGCGCGGTGGGTGGCGGC 3651
QY 3661 GCTACGGCGAGGAACTCGTCAATGTTGCATAGAGCTTTGATCTACATGA 3717
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RESULT 7
US-10-692-556-5
; Sequence 5, Application US/10692556
; Publication No. US20040115623A1
; GENERAL INFORMATION:
; APPLICANT: Homa, Fred
; APPLICANT: Wathen, Michael
; APPLICANT: Hopkins, Todd
; APPLICANT: Thomsen, Darrell
; TITLE OF INVENTION: A Method for Treating Herpes Virus
; FILE REFERENCE: 00221
; CURRENT APPLICATION NUMBER: US/10/692,556
; CURRENT FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 3708
; TYPE: DNA
; ORGANISM: herpes simplex
US-10-692-556-5

Query Match 82.3%; Score 3059.8; DB 19; Length 3708;
Best Local Similarity 89.3%; Pred. No. 0;
Matches 3321; Conservative 0; Mismatches 387; Indels 9; Gaps 2;

QY 1 ATGTTTGTGCGCGGGGCGGCGGCTTCCCGGGGGGAGTCCGGGGCTCGGGCGGCG 60
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DB 61 TCGGGTTTTCGCGCGCGCGGCGGCTTCCGGAGCGGCGGCGGCGGCGGCGGCGGCTTGT 117
QY 121 CGCCGCGCAGAACTTCAACCCCACTCGCTCAGACCGGAAACGAGCAAGAGCGCCCG 180
DB 118 TTGAGGCAAACTTTTACAACTTACCTCGCCCGGAGTCCGGACGCAAGAGCGGACG 177
QY 181 GGGCGGCTCAGCGGCATACGTAATACGAGAGTCCGAGAAATTCGATTCGCGCCG 240
DB 178 GGGCAACCCAGCGGCATACGTAATACGAGAAATTCGATTCGATTCGATTCGCGCGG 237
QY 241 GCTTCGCTGAGAGAGCGCCCGCGGAGAGCGCACCGGGTCCAGAGCGCGCGCTC 300
DB 238 CGGGTCTGAGAGAGTCCCGCGGAGAGAGCGCGCGGGTCCAGAGCGGTCACTC 297
QY 301 CGCGCGCGCTTAAAGTGTACTGCGGGGGGAGAGCGAGCTCTCGCGCTGGGGCGG 360
DB 298 AAGCGCGCGCCCAAGGTGTACTGCGGGGGGAGAGCGAGCTCTCGCGCTGGGTGCG 357
QY 361 GAGGCTTCTGCGCGGCTCGCTTGGCGCTGTGGGGCGGTGGGACCATGCCCGCCCAAGGG 420

DB 358 GCGCGGCTTTCGCGCGCGGCGCTCGCGCTGTGGGGCGGCTGGACCAACGCGCCCGCGGGG 417
QY 421 TTTCGACCCCAACCGTCAACCGTCTTCAGAGTGACGATCCTCGAGAGCAAGTGGAAACACGCG 480
DB 418 TTCAACCCCAACCGTCAACCGTCTTCAGAGTGACGATCCTCGAGAGCAAGTGGAGACGCG 477
QY 481 TACAGATGCGCGCGCCCGAGCTCAACGAGCGATTTATGAGCGCCATCAACCGAGCGG 540
DB 478 TACGCGATGCGCGCGCGCGAGTTCCAGCGCGGTTTATGAGCGCCATCAACCGAGCGG 537
QY 541 ACCGTATCAACCGTCTGGGTCTGACCCCGGAGGCGATCGCGTTCGCGCTTCACTCTAC 600
DB 538 ACCGTATCAACCGTCTGGGTCTGACCCCGGAGGCGATCGCGTTCGCGCTTCACTCTAC 597
QY 601 GGCACGCGCGAGTCTTTTACATGAACGAGCGAGGTGATCGGCACCTGACGAGTCCGCT 660
DB 598 GGCACGCGCGAGTCTTTTACATGAACGAGCGAGGTGATCGGCACCTTACATGCCG 657
QY 661 GCGCGCGCGATCTCTCGAGCGCTTGGCGCGGCTTGGCGAGTTCGCGGGGGCGTTCG 720
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DB 718 TTTCGCGCGATCTTCGCGGACCACTTCGAGGCGAGGTGGTGGAGCGCGCACCGAGCTGATC 777
QY 781 TATTACGAAACGCGCGCGGCTTTCGCGCGGATCAGGAAAGTACGAGGGGGCGCTCGACGCC 840
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QY 841 GCCTACCTGTGCGCAACTTTTTCGCGCGGATCAGGAAAGTACGAGGGGGCGCTCGACGCC 900
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DB 898 ACCACCGGTTTATCTCGGACAAACCGGGGTTTGTCACTTCGCGGTGATCGCGCTCAAA 957
QY 961 CCGCGCGCGGAGCGCGCGCGGCGCAACCGCGCGGCGCGCGGCTTCGGAACCTCGAGC 1020
DB 958 CCGGGCGGAGCAACACGCTAGCGCGCGGCGCGGCTTCGGAACCTCGAGC 1017
QY 1021 GACGTCGAGTTTAACTGACGCGCGGACCAACTTCGCGGCTCGAGGGGGCGCTTGTGACCTG 1080
DB 1018 GACGTCGAGTTTAACTGACGCGCGGACCAACTTCGCGGCTCGAGGGGGCGCTTGTGACCTG 1077
QY 1081 CCGGCTTCAAGCTCATGTCTTCGATTCGAAATGCAAGGCGCGGGGGAGAGCAGCTG 1140
DB 1078 CCGGCTTCAAGCTCATGTCTTCGATTCGAAATGCAAGGCGCGGGGGAGAGCAGCTG 1137
QY 1141 GCCTTTCGCGTCGCGGAGCGCGCGGCGGCGGCGGCTTCGGAACCTCGAGC 1200
DB 1138 GCCTTTCGCGTCGCGGAGCGCGCGGCGGCGGCTTCGGAACCTTCGATTCGATTCGCTCTAC 1197
QY 1201 GACCTGTCCACACCGCGCTTCGAGCACTCTCTCTGTTTTCGCTCGATTCCTCGACCTC 1260
DB 1198 GACCTGTCCACACCGCGCTTCGAGCACTCTCTCTGTTTTCGCTCGATTCCTCGACCTC 1257
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DB 1258 CCGGAAATCCCACTGAAACGAGCTGCGGCGGCGGCGGCTTCGCGCGCGGCTTCGGA 1317
QY 1321 TTTGACGAGAAATTCGAGATGCTGCGCTTCATGACCTTCGATTCGATTCGATTCGATTCG 1380
DB 1318 TTTGACGAGAAATTCGAGATGCTGTTGGCTTCATGACCTTCGATTCGATTCGATTCGATTCG 1377
QY 1381 GAGTTCGTGACCGGGTACAAACATCAATCAATTCGAGTGGCGCTTCGCTTCGACCAAGCTG 1440
DB 1378 GAGTTCGTGACCGGGTACAAACATCAATCAATTCGAGTGGCGCTTCGCTTCGCGCAAGT 1437
QY 1441 ACGAGATCTTAAAGTTCGCGCTCGAGCGGTTCGCGGCGCATGAACCGCGGGGTGTTC 1500
DB 1438 ACGGACATTTTAAAGTTCGCGCTCGAGCGGTTCGCGGCGCATGAACCGCGGGGTGTTC 1497

QY	1501	CGCGTGGGACATCGGCAGAGCCATCTTCAGAAAGCGCAGCAAGATCAAGGTGAACGGG	1560
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QY	1561	ATGCTGAACATCGACATGTACGGCATCATCAACGACAAAGGTCAAACTCTCCAGCTACAAG	1620
Db	1558	ATGCTGAACATCGACATGTACGGCATCATCAACGACAAAGATCAAGCTCTCGAGCTACAAG	1617
QY	1621	CTGAACGCGCTCGCCGAGCGCTCTTGAAGGACAAAGAAAGATCTGAGCTACCGGCAC	1680
Db	1618	CTCAACGCGCTGGCCGAAGCCGTCTTGAAGGACAAAGAAAGATCTGAGCTACCGGCAC	1677
QY	1681	ATCCCGGCTACTAGCGCTCGGGCCCGCGCAGCGCGGGGTGATCGGGAGTATTGTG	1740
Db	1678	ATCCCGGCTACTAGCGCGCGGGCCCGCGCAACCGGGGTGATCGGGAGTACTGCATA	1737
QY	1741	CAGGACTCGCTGCTGGTGGGCAGCTGTTCTTCAAGTTTTCTGCGCACCTGGAGCTTTCC	1800
Db	1738	CAGGATTCCTGCTGCTGGGCAGCTGTTTAAAGTTTTTGGCCCATCTGGAGCTCTCG	1797
QY	1801	GCCTCGCGCCCTGGCGGGGATCAACATCAACCGCACCATCTACGACGGCCAGCATC	1860
Db	1798	GCCTCGCGCCCTGGCGGGGTAAATAACATCAACCGCACCATCTACGACGGCCAGCATC	1857
QY	1861	CGGCTCTTCAGTGCCTCTCGGCTTTCGGGGCAGAAAGGCTTCATCTGCGGCACAC	1920
Db	1858	CGGCTCTTACGTGCTCTGCGCTTGGCCGACAGAAAGGCTTTTATCTGCGGCACAC	1917
QY	1921	CAGGGGCGTTTTGGGGCTCGACAAAGAGCGGCCCAAGCGCCCGCGCTGCCCTCGGGG	1980
Db	1918	CAGGGGCGATTTAGGGGCGCCGGGGGAGGCGCCCAAGCGTCCGCGCGAGCCCGGAG	1977
QY	1981	GAAGGGAGCGCCGGGGGACGGGAAACGGGACAGAGGATAAGGACGACGAGGACGAG	2040
Db	1978	GACGAGGAGCGCCAGAGGAGGAGGGGAGGAGC-----AGGACGAACGAGGAGGGC	2031
QY	2041	GACGGGACGAGCGGAGGAGGTTCGCGCGCAGACACGGGGCCGGCAGCTTGGGTACGAG	2100
Db	2032	GGGGCGGAGCGGAGCGCGAGGCGCGCGGAGACCGCGCCGGCAGCTGGGGTACCAG	2091
QY	2101	GGGGCGGGTCTTCGACCCACCTTCGGGTTTTACGTCGACCCCGTGGTGGTTTTGAC	2160
Db	2092	GGGGCGAGGTTCTTGACCCCACTTCGGGTTTTACGTGAACCCCGTGGTGGTTTCGAC	2151
QY	2161	TTTGCCAGCTGTATCCCGAGCATCATCCAGGCCCAACACTGTGCTTCAGTACGCTCTCC	2220
Db	2152	TTTGCCAGCTGTATCCCGAGCATCATCCAGGCCCAACACTGTGCTTCAGCACGCTCTCC	2211
QY	2221	CTCGGGCCGAGCGCGTTCGCGACCTTGAGGCGGACCGGGACTACTGGAGATCGAGTG	2280
Db	2212	CTGAGGGCCGACGAGTGGCGCATCTGAGGCGGGCAAGGACTACTGGAGATCGAGTG	2271
QY	2281	GGGGCGCAGCGCTGTTCTTCTGTAAGGCCACAGTACGCGAGAGCTCTCTCAGCATCTG	2340
Db	2272	GGGGCGCAGCGCTGTTCTTCTGTAAGGCCACAGTACGCGAGAGCTCTCTCAGCATCTC	2331
QY	2341	CTCGCGCATGTGGTGGCCATCGAAAGCAGATCCGCTCGCGGATCCCCCAGACACCCCC	2400
Db	2332	CTCGGGACTGGCTCGCCATCGAAAGCAGATCCGCTCGCGGATTTCCCCAGACGACCCC	2391
QY	2401	GAGGAGCGCTCTCTCTCGACAGCAACAGGCGGCATCAAGGTGGTGTGCACTCGTG	2460
Db	2392	GAGGAGCGCTGCTCTGGAACAGCAGCAGCGCCGCATCAAGGTGGTGTGAACTCGTG	2451
QY	2461	TACGGTTTACCGGGCGCAGCAGGCTCTCTGCGCTGCTGCACTGGCGCGCCACCGTG	2520
Db	2452	TACGGTTTACCGGGAGCGCAGCAGGACTCTCTGCGCTGCTGCACTGGCGCGCAGCGTG	2511
QY	2521	ACGACCATCGGCGCAGATGCTCTCTCGCAGCGCGCTACGTTACGCGCGCTGGGCG	2580
Db	2512	ACGACCATCGGCGCGAGATGCTGCTCGCGACCCGCGAGTACGTTCCACGCGCGCTGGCG	2571

QY	2581	GAGTTGATCAGCTGCTGGCCGCACTTTCCGAGGCGCGCCGATGCGCGCCCCCGGTCG	2640
Db	2572	GCCTTCGAAAGCTCTCTGGCCGATTTCCCGAGGCGCGCCGACATGCGGCCCCCGGGCC	2631
QY	2641	TACTTCATGGGCATCATCTACGGGGACACGAGCTCCATTTTTCGTTTTGTGCGCGGCTC	2700
Db	2632	TATTCATGCGCATCATCTACGGGGACACGAGCTCCATATTTTGTGCTGTGCGCGGCTC	2691
QY	2701	ACGGCCCGGGCTGTGTGGCCATGCGGGGACAAAGTGGCGAGCACAATCTCGCGCGGCTG	2760
Db	2692	ACGGCCCGGGCTGTGACGGCCATGCGGGGACAAAGTGGCGAGCCACATCTCGCGCGGCTG	2751
QY	2761	TTCTCTCCCGCATCAAGCTCGAGTGCAGAAACGTTTCCAAAGCTGTCTCATCGCC	2820
Db	2752	TTTCTGCCCCCATCAAACTCGAGTGCAGAAAGCTTCAACAAAGCTGTCTCATCGCC	2811
QY	2821	AAGAAAAAGTACATCGGCGCTCATCTCGGGGGCAAGATGCTCATCAAGGGCGTGGATCTG	2880
Db	2812	AAGAAAAAGTACATCGGCGCTCATCTACGGGGTAAAGTGTCTCATCAAGGGCGTGGATCTG	2871
QY	2881	GTGCGAAAAAACAATCGGCGTTCATCAACGCGACCTCCAGGGCCCTGGTGCAGCTGCTG	2940
Db	2872	GTGCGAAAAAACAATCGGCGTTCATCAACGCGACCTCCAGGGCCCTGGTGCAGCTGCTG	2931
QY	2941	TTTTACGACGATACCGTATCCGAGGCGCGCGCGTTCAGCGAGCGCCCCGACAGAGAG	3000
Db	2932	TTTTACGACGATACCGTATCCGAGGCGCGCGCGTTCAGCGAGCGCCCCGACAGAGAG	2991
QY	3001	TGGTGGCGGACCCCTGCGCGGAGGAGCTGCGAGCGTTTCGCGGGCGTCTCTGTAGAGGCC	3060
Db	2992	TGGTGGCGGACCCCTGCGCGGAGGAGCTGCGAGCGTTCGCGGGCGTCTCTGTAGAGGCC	3051
QY	3061	CATCGGCGATACCGGACCGGAGAGGAGCATCAGAGCTTTGTCTCACCGCGCAACTG	3120
Db	3052	CATCGGCGATACCGGACCGGAGAGGAGCATCAGAGCTTTGTCTCACCGCGCAACTG	3111
QY	3121	AGCAGACCCCGCGCGGTACACCAACAGCGCTGCGCCACCTGACGCTGTTATTACAAG	3180
Db	3112	AGCAGACCCCGCGCGGTACACCAACAGCGCTTGGCCACCTGACGCTGTTATTACAAG	3171
QY	3181	CTCATGCGCGCGCGCGGAGGTCCCTGCCATCAAGGACCGGATCCCGTACGTTGATCGTG	3240
Db	3172	CTCATGCGCGCGCGCGGAGGTCCCGTCCATCAAGGACCGGATCCCGTACGTTGATCGTG	3231
QY	3241	GCCCAGACCCCGGAGGTAGAGGAGACGTCGCGCGGTGTCGCGCCCTCCGCGAGCTAGAC	3300
Db	3232	GCCCAGACCCCGGAGGTAGAGGAGACGTCGCGCGGTGTCGCGCCCTCCGCGAGCTAGAC	3291
QY	3301	GCGCGCCCGCAGGGGACGAGCCCGCCCCCAGCGCCCTGCGCTCCCGCGCCAAAGCGC	3360
Db	3292	GCGCGCCCGCAGGGGACGAGCCCGCCCCCAGCGCCCTGCGCTCCCGCGCCAAAGCGC	3351
QY	3361	CCCCGGGAGACCGCGTTCGCATGCGGACCCCGCGGAGCGCGTCCAAAGCCCGCAAGGTG	3420
Db	3352	CCCCGGGAGACCGCGTTCGCATGCGGACCCCGCGGAGCGCGTCCAAAGCCCGCAAGGTG	3411
QY	3421	CTGTGTTCGAGCTGGCGGAGGATCCCGGGTACCGCATCGCCCGCGGGGGTTCGCTCAAC	3480
Db	3412	CTGTGTTCGAGCTGGCGGAGGATCCCGGGTACCGCATCGCCCGCGGGGGTTCGCTCAAC	3471
QY	3481	ACGACTATTACTTCTCGCACTCTGGGGGCGGCTTCGCTGAGAGTTTCAAGGGCCCTGTTT	3540
Db	3472	ACGACTATTACTTCTCCACCTGTGGGGGCGGCTGCTGAGATTCNAAGGCTCTGTT	3531
QY	3541	GGAAATAACGCAAGATCACCGAGAGTCTGTTAAAGAGGTTTATTCGCGAGACGTTGGAC	3600
Db	3532	GGGAATAACGCAAGATCACCGAGAGTCTGTTAAAGAGGTTTATTCGCGAGTGTGGCAC	3591
QY	3601	CCCCCGGAGCAGCTGGCGCGCGGCTCAGGGCCCGGGGTTTCGGGCGCGCGGGCGCGGC	3660
Db	3592	CCCCCGGAGCAGCTGGCGCGCGGCTCAGGGCCCGGGGTTTCGGGCGCGCGGGCGCGGC	3651
QY	3661	GCTACGGCGGAGGAACTCGTCGAATGTTGATAGAGCCTTTTGATACTCTAGCATGA	3717

QY 121 CGCCGCGAGAACTTCTACAACCCCACTCGCTCAGACCGGAACGAGCAAGGCCGCC 180
DB 118 TTGAGGCAAACTTTTACAACCCCTACCTCGCCCGAGTCGGAGCGCAACAGAAAGCGGACC 177
QY 181 GGGCCGGCTCAGCGGCATAGCTACTACAGCGAGTGGAGCAATTTTCGATTTATCGCCCG 240
DB 178 GGGCAAAACCGCGGCATAGCTACTATAGCAATGCGATGAATTTTCGATTTATCGCCCG 237
QY 241 CGTTCTGCTGAGAGAGAGCCCGCGAGCAGCGCACCGGGGTCCAGACGGCGCCCTC 300
DB 238 CGGGTCTGAGAGAGATGCCCGCGAGAGCGCGCGGGTGGACACGGTCACTTC 297
QY 301 CGGCGGCGCCCTAAGGTGTAATGCGGGGGAGAGCGCGAGCTCTCCGCTGGGCGCG 360
DB 298 AAGCGCGCCCCAAGGTGTAATGCGGGGGAGAGCGCGAGCTCTCCGCGTGGGTG 357
QY 361 GAGGGCTTCTGCGCGGTCTGCTGCGCTGCGGGGGTGGAGCATGCCCCCAAGGG 420
DB 358 GCGGGCTTCTGCGCGCGGTCTGCGCGCTGCGGGGGAGAGCGCGAGCTCTCCGCGTGGGTG 417
QY 421 TTTCGACCCCAACCGTCAACCGTCTTCAAGGTGACGACATCTCGAGCAGCTGGAACACGCG 480
DB 418 TTCAACCCCAACCGTCAACCGTCTTCAAGGTGACGACATCTCGAGCAAGTGGAGCAGCG 477
QY 481 TACAGCATGCGCGCCCGCAGCTCCAAGCGGATTTATGAGCGCCATCACGCCCGCGGG 540
DB 478 TACGGCATGCGCGCGCCCGTTCACGCGCGGTTTATGAGCGCCATCACACCGAGGG 537
QY 541 ACCGTATCATCGCTTCTGGTCTGACCCCGAAGGCGCATCGGGTCCGGTTCACTGTAC 600
DB 538 ACCGTATCATCGCTTCTGGTCTGACCCCGAAGGCGCATCGGGTGGCGGTTTCACTGTAC 597
QY 601 GGCAGCGCGAGTACTTTTACATGAACAGGCGAGGTGATCGGCACCTCGAGTGGCT 660
DB 598 GGCAGCGCGAGTACTTTTACATGAACAGGCGAGGTGATCGGCACCTCAATGCGCG 657
QY 661 GCGCGCGAGTCTCTGCGAGCGCTTGGCGCGCCCTCGCGAGTCCGCGGGCGGTG 720
DB 658 GCGCGCGAGTCTCTGCGAGCGCATGCGCGCGCCCTCGCGAGTCCGCGGGCGGTG 717
QY 721 TTCGGCGGATCTCGCGGACACCTTCAGAGCGAGGTGGAGCGCGCGCATCGGTAC 780
DB 718 TTCGGCGGATCTCGCGGACACCTTCAGAGCGAGGTGGAGCGCGCATCGGTAC 777
QY 781 TATTACGAAACGCGCGGACCTGTAACCGCTTCTGTCGAGAGCGCGCGCTG 840
DB 778 TACTACGAGACGCGCGGCTCTGTTTACCGCGTCTACGTCGAGCGCGCGGTGCTG 837
QY 841 GCCTACCTGTGCGACAACTTTTGGCCCGCGATCAGGAAGTACGAGGGGGGTTCGACGCC 900
DB 838 TCGTACCTGTGCGACAACTTTGCGCCCGCATCAAGAGTACGAGGTGGGTTCGACGCC 897
QY 901 ACCACCGGTTATCTCGTGAACACCGGGGTTTGTCACTTCGCGTGTGTAACGCGCTCAAG 960
DB 898 ACCACCGGTTATCTCGTGAACACCGGGGTTTGTCACTTCGCGTGTGTAACGCTCAAA 957
QY 961 CCGGCGCGGGAACGCGCGCGCAACCGCGCCCCCGAGCGGCTTCGGAACCTCGAGC 1020
DB 958 CCGGCGCGGGAACCAACCGCTAGCCCGCGGGCCCCGATGGCTTCGGAACATCCAGC 1017
QY 1021 GACGTCGAGTTTAACTGACCGCGGCAACACTTGGCGGTTCGAGGGGGCCATGTGTGACCTG 1080
DB 1018 GATGTCGAGTTTAACTGTCGCGGCAACACTTGGCCATCGAGGGGGCATGAGCGACTA 1077
QY 1081 CCGGCTTACAGCTCATGTGCTTCGATATCGAATCGAAGCGCGGGGGAGAGAGAGCTG 1140
DB 1078 CCGGCTTACAGCTCATGTGCTTCGATATCGAATCGAAGCGGGGGAGAGAGAGCTG 1137
QY 1141 GCCTTTCGCTGCGGGAACCGCGGAGACCTCGTCAACGAGTCTCTGCTCTAC 1200
DB 1138 GCCTTTCGCTGCGGGGCAACCGGAGACCTGGTCAACGAGATATCTGCTCTCTAC 1197

QY 1201 GACCTGTCCACCAACCGCCCTCGAGCACATCTCTCTGTTTTCGTCGGATCTCGACCTC 1260
DB 1198 GACCTGTCCACCAACCGCCCTCGAGCACATCTCTCTGTTTTCGTCGGTCTCTCGACCTC 1257
QY 1261 CCGAGTCCCACCTCAGCGATCTCCCTCCAGGGGCTCGCGGCCCTCGTCTCTGAG 1320
DB 1258 CCGGAATCCACCTCAGCGAGCTCGCGGCTCGAGGGCTCGCCACCGCCCTGCTTCTGGA 1317
QY 1321 TTTGACGCGAATTCGAGATCTGCTGCGCTTCATGACCTTCGTCGTCGTCGTCGAGT 1380
DB 1318 TTGACGCGAATTCGAGATCTGCTGCGCTTCATGACCTTCGTCGTCGTCGTCGAGT 1377
QY 1381 GAGTTCGTGACCGGGTACAACATCAATCAATTCGACTGCGCTTCGTCGTCGTCGAGT 1440
DB 1378 GAGTTCGTGACCGGGTACAACATCAATCAATTCGACTGCGCTTCGTCGTCGTCGAGT 1437
QY 1441 ACGGAGATCTACAAGGTCCCGCTCAGCGGTACCGGGGATGAACCGCGGGGTGTTTC 1500
DB 1438 ACGGACATTTACAAGGTCCCGCTCAGCGGTACCGGGGATGAACCGCGGGGTGTTTC 1497
QY 1501 CGCGTTCGGGACATCGCGCAGAGCCACTTTCAGAGCGCAGCAAGATCAAGGTGAACGG 1560
DB 1498 CGCGTTCGGGACATAGCGCAGAGCCACTTTCAGAGCGCAGCAAGATCAAGGTGAACGG 1557
QY 1561 ATGTGAAATCGAATGTACGGCATCATCAACCGAAGAGGTCAAACTCTCCAGCTACAAG 1620
DB 1558 ATGTGAAATCGAATGTACGGCATCATCAACCGAAGATCAAGCTCTCGAGCTACAAG 1617
QY 1621 CTGAACCGCGTTCGCGAGGCGCTCTTGAAGGACAAGAAAGAGATCTGAGCTACCGGAC 1680
DB 1618 CTGAACCGCGTTCGCGAGGCGCTCTTGAAGGACAAGAAAGAGATCTGAGCTATCGGAC 1677
QY 1681 ATCCCGCTACTAGCTTCGCGCGCCCGCGAGCGCGGGGTGATCGCGAGTATTTGTG 1740
DB 1678 ATCCCGCTACTAGCTTCGCGCGCCCGCGAGCGCGGGGTGATCGCGAGTATTTGTG 1737
QY 1741 CAGGATCTGCTGCTGCTGCGGCGAGCTGTTCTTCAAGTTTCTGCCACCTCTGAGCTTTCC 1800
DB 1738 CAGGATCTGCTGCTGCTGCGGCGAGCTGTTTAAAGTTTTCGCCCATCTGAGCTCTCG 1797
QY 1801 GCGTTCGCGCGCTTCGCGGGGATCAACATCAACCGCACATCTACGACGGCCAGAGATC 1860
DB 1798 GCGTTCGCGCGCTTCGCGGGGTATTAACATCAACCGCACATCTACGACGGCCAGAGATC 1857
QY 1861 GCGCTTTACGCTCTCTGCGCTTCGCGGCGCAGAGGGCTTCATCTCTCGCGACACC 1920
DB 1858 GCGCTTTACGCTCTCTGCGCTTCGCGCGCAGAGGGGTATTTCTCTGCGGACACC 1917
QY 1921 CAGGGCGGTTTCTGCGGCGCTTCGACAAAGAGGCGCCCAAGCGCCCGCGCTCTCGGGG 1980
DB 1918 CAGGGCGGTTTACGGGCGCCCGGGGGAGGGGCCCAAGCGTCCGGCCGACGCCGGAG 1977
QY 1981 GAAGGGAGCGCGCGGGGAGCGGGAACCGGGAACGAGGATAAGGACGACGACGAGACGAG 2040
DB 1978 GACGAGGAGCGCGCAGAGGAGGGGAGGAGCG-----AGAACGAAACGCGAGGAGGCG 2031
QY 2041 GACGGGAGCAGCGCGAGGAGGTTCGCGCGCAGACCGGGGCGCGACAGTTGGGTACCAG 2100
DB 2032 GGGGCGAGCGGGAGCGCGAGGGCGCGGGAGACCGCGCGCGGCGACAGTGGGGTACCAG 2091
QY 2101 GGGGCGCGGGTCTCTGACACCCACCTCTCGGGTTTTCAGCTCGACCCCGTGTGTGTTGAC 2160
DB 2092 GGGGCGAGGGTCTCTGACACCCACCTCTCGGGTTTTCAGCTGNAACCCCGTGTGTGTTGAC 2151
QY 2161 TTTGCGAGCTGTATCCCGAGCATCATCAGGGCCCAACCTGTGTGTTGAGTACGCTCTCC 2220
DB 2152 TTTGCGAGCTGTATCCCGAGCATCATCAGGGCCCAACCTGTGTGTTGAGTACGAGTGTG 2211
QY 2221 CTGCGGCGCGAGGCGCTCGCGCACTTCGAGGCGGACCGGGACTACCTCGAGATCGAGGTG 2280
DB 2212 CTGAGGCGCGAGCAGTGGGCGCATCTGAGGCGGGCAAGGACTACCTCGAGATCGAGGTG 2271
QY 2281 GGGGCGCGAGCGGCTGTTCTTCTGTAAGAGGCCCAAGTACGCGAGAGCGCTCTGAGCATCCTG 2340

Db	358	GGCGGCTTCTGGCGCGCGCTCGCGCTGTGGGGCGCGGTGGACCAACGCCCGCGGGGG	417
Qy	421	TTGCACCCCACCGTCAACCGTCTTCCACGTGTACACATCTCTGGAGCACGTGGAAACACGCG	480
Db	418	TTCAACCCACCGTCAACCGTCTTTCACGTGTATGACATCTCTGGAGAACGTGGAGCACGCG	477
Qy	481	TACAGCATGGCGCGCGCCAGCTCCAGAGGATTTATGACGCCATACGCCCGCGCGG	540
Db	478	TACGGCATGGCGCGCGGCCAGTTCACCGCGCGTATTGACGCGCATCACACGACGCGG	537
Qy	541	ACCGTCATACGCTTCTGGGTCTCACCCCGAAGGCCATCGGTCGCGCGTTCAGTCTAC	600
Db	538	ACCGTCATACGCTCTTGGGCTGACTCCGGAAGGCCACCGGTGGCGGTTTACGTTTAC	597
Qy	601	GGCACGGCGAGTACTTTTATCATGAACAAGCGAGGTGGATCGGCACCTTCAGTGCCTG	660
Db	598	GGCACGGCGAGTACTTTTATCATGAACAAGGAGGAGTTGACAGGCACCTACATGCGCG	657
Qy	661	GCCCGCGCGATCTCTGGAGCGCTCGCGCGCGCCCTGCGCGAGTCCGCGGGGGGTG	720
Db	658	GCCCGACGAGATCTCTCGAGCGCATGCGCGCGCGCCCTGCGCGAGTCCCGGGCGGTG	717
Qy	721	TTCCGCGGCATCTCCGCGGACCACTTCGAGCGGAGGTGTGGAGCGCGCGGACGTGTAC	780
Db	718	TTCCGCGGCATCTCCGCGGACCACTTCGAGCGGAGGTGTGGAGCGCGCACCGAGCTGTAC	777
Qy	781	TATTTACGAACCGCGCCGACCCCTGTACTACCGCTCTTCTGTGCGAAGCGGGCGCGCTG	840
Db	778	TACTACGAGACGCGCCCGCTCTGTTTTACCGGTCTACGTCCGAGCGGGCGGTGTCTG	837
Qy	841	GCCTACTGTGCGCAAACTTTTGGCCCCCGCATCAGGAAGTACGAGGGGGCGTCGACGCC	900
Db	838	TCGTACTGTGCGCAAACTTCTGCCCGCCATCAAGAAGTACGAGGGGTGGGGTCGACGCC	897
Qy	901	ACCACCCGGTTATCTTGGAACAACCCGGGTTTGTACCTTCGGCTGGTACCGCTCAAG	960
Db	898	ACCACCCGGTTCACTCTTGGAACAACCCGGGTTGTGTACCTTCGGCTGGTACCGTCAAA	957
Qy	961	CCGGCGCGGGAAACCGCGGCCAACCGCGCCCCCGACGCGGTTTCGGAACCTCGAGC	1020
Db	958	CCGGCGCGGAACAACAGCTAGCCAGCCGCGGGCCCCGATGGCTTCGGGACATCAGC	1017
Qy	1021	GACGTCAAGTTTAACTGCACGGCGGAACAACCTGGCCGTTCGAGGGGGCCATGTGTGACCTG	1080
Db	1018	GATGTCAAGTTTAACTGTACGGCGGAACAACCTGGCCCATCGAGGGGGCATGACGACCTA	1077
Qy	1081	CCGGCTTCAAGCTCATGTGTTTCGATATCGAATGGAAGCCGGGGGGGAGGACGAGCTG	1140
Db	1078	CCGSCATACAAGCTCATGTGTTTCGATATCGAATGCAAGCGGGGGGGGAGGACGAGCTG	1137
Qy	1141	GCCTTTCGGGTTCGGGAACCGCGGAAGACCTGTCTATCCAGATCTCTGTCTGTCTTAC	1200
Db	1138	GCCTTTCGGGTTCGGGGACCCCGGAGGACCTGTCTATCCAGATATCTGTCTGTCTTAC	1197
Qy	1201	GACCTGTCCACCAACCGCCCTCGAGCACATCCTCTGTCTTCGCTCGGATCCTCGGACCTC	1260
Db	1198	GACCTGTCCACCAACCGCCCTCGAGCAGTCTCTGTCTTCGCTCGGTTCTCGGACCTC	1257
Qy	1261	CCGAGTCCCAACCTCAGCGATCTGCGCTCAGGGGCGCTGCGGCCCGCCGCTCGCTTGAG	1320
Db	1258	CCGGAATCCCAACCTGAACGAGCTGGCGGCGAGGGGCGTCCCAACCGCGTGTCTTGAA	1317
Qy	1321	TTTGACAGCGAATTCGAGATGCTGTGGCTTTCATGACCTTCGTCAAGCAGTACGGCCCC	1380
Db	1318	TTTGACAGCGAATTCGAGATGCTGTGGCTTTCATGACCTTCGTCAAGCAGTACGGCCCC	1377
Qy	1381	GAGTTCTGAGCCGGGTACAACATCATCACTTCGACTGGGCCCTTCGTCTGTGACCAAGCTG	1440
Db	1378	GAGTTCTGAGCCGGGTACAACATCACTTCGACTGGGCCCTTCGTCTGTGCGCAAGCTG	1437
Qy	1441	ACGAGATCTACAAGGTCCCGCTCGACGGGTACGGGCGCATGAACGCGCGGGGTGTGTTTC	1500

1438	DB	ACGAGACATTTACAAGGTCCCCCTGGACGGGTACGGCCGCATGAACGGCCGGGGCGGTGTTT	1499
1501	QY	CGCGTGTGGGACATCGGCCAGAGCCACTTTTCAGAAGCGCAGCAAGATCAAGGTGAACCGGG	1560
1498	DB	CGCGTGTGGGACATAGGCCAGAGCCACTTCCAGAGCGCAGCAAGATAAAGGTGAACCGCC	1557
1561	QY	ATGSGTGAACATCGACATGTACGGGATCATCACCGACMAAGSTCAAACTCTCCAGCTACAAG	1520
1558	DB	ATGSGTGAACATCGACATGTACGGGATTTATAACCGACAAGATCAAGCTCTCGAGCTACAAG	1617
1621	QY	CTGAACCCCGTGCGCCAGGCGCTCTTGAAGGACAAGAAGAAGGATCTGAGCTACCCGCAC	1680
1618	DB	CTAACCGCGTGGCCGAAGCCGCTCTGAAGGACAAGAAGAAGCACTTGAAGCTATCCGGAC	1677
1681	QY	ATCCCCCGCTACTACGCTCTCCGGGCCCGCAGCGGGGTGATCGGCCAGTATTGTGTG	1740
1678	DB	ATCCCCACCTACTACGCGCGCGGCCCGCGCAACGGGGGTGATCGGGAGTACTGCATA	1737
1741	QY	CAGACATCGCTGTGTGTGGGCAAGCTGTCTTCAAAGTTTCTGCCGACCTTGGAGCTTTTCC	1800
1738	DB	CAGGATTTCCCTGTGTGTGGCCAGCTGTCTTTTAAAGTTTGTGCCCATCTCTGGAGCTCTCG	1797
1801	QY	GCGGTGCGCGGCTGTGGGGCATCAATCACCGGCACCATCTTACGACGCCAGCAGATC	1860
1798	DB	GCCGTGCGCGGCTTGGCGGTATTAACATCACCCGCACCATCTACGACGCCAGCAGATC	1857
1861	QY	CGCGTCTTCACTGCTCTCTGCGGCTTGGCGGCGCAGAAGGCTTCATCTCTGCCGACACC	1920
1858	DB	CGCGTCTTTAGTGTGCTGTGCGCTGTGGCGGAGCGCCCAAGCGCTCGCGCGCAGCCCGGAG	1917
1921	QY	CAGGGCGGTTTCGGGGCTTCGACAAAGAGGCGCCCAAGCGCCCGCTGCTCGGGGG	1980
1918	DB	CAGGGCGGATTTAGGGCGCGCGGGGAGGCGCCCAAGCGCTCGCGCGCAGCCCGGAG	1977
1981	QY	GAAGGAGAGCGCCCGGGGACGGGAAACGGGGACGAGGATAAGACGACGACGAGGACGAG	2040
1978	DB	GACGAGAGCGGCCAGAGGAGGAGGGGGAGGACG-----AGAAACGAAACGCGAGGAGGGC	2031
2041	QY	GACGGGACGAGCGCGAGGAGGTGCGCGCGGACCGGGGCGCGGACGTTGGGTACCGAG	2100
2032	DB	GGGGCGAGCGGGAGCCGGAGGGCGCGGGAGACCGCGCGCGGACGTTGGGGTACCGAG	2091
2101	QY	GGGGCCCGGTCTCTGACCCCACTCCGGGTTCACGTGACACCCCGTGGTGGTGTGTTGAC	2160
2092	DB	GGGGCCAGGGTCTTTGACCCCACTTCCTCGGGTTCACGTGAACCCCGTGGTGGTGTTCGAC	2151
2161	QY	TTTGGCAGCCTGTATCCCGACGATCATCGAGGCCCAAACTGTGCTTCAGTACGCTCTCC	2220
2152	DB	TTTGTCCAGCCTGTATCCCGACGATCATCCAGGCCCAACAACCTGTGTCTTCAGCAGCTCTCC	2211
2221	QY	CTGGGGCCGAGCGGTGCGGACCTTGGAGGGGACCGGGGACTACCTGGAGATCGAGGTG	2280
2212	DB	CTHAGGGCCGACGAGTGGCGCACTTGGAGCGGGCAAGGACTACTCTGGAGATCGAGGTG	2271
2281	QY	GGGGGCCGACCGGCTGTTCTTCGTGAAGGGCCACGTACGGGAGAGCCTGTGTGAGCATCTTG	2340
2272	DB	GGGGGCCGACCGGCTGTTCTTCGTCAAGGCTCACGTGCGAGAGAGCCTCTCTCAGATCTCTC	2331
2341	QY	CTGCGGACTGTGCTGGCCATATGCAAAACGAGATCCGCTCGCGGATCCCCCAGAGCACCCCC	2400
2332	DB	CTGCGGACTGTGCTGCAATGCGAAAGCAGATCCGCTCGCGGATTTCCCCCAGAGCACCCCC	2391
2401	QY	GAGGAGCCGCTCTCTCGACAGCAACAGGGCGCCATCAAGGTGTGTGTGCACTCGGTG	2460
2392	DB	GAGGAGCCGCTGCTCTTGGACAAGACAGCGCCCATCAAGGTGCTGTGTAACTCGGTT	2451
2461	QY	TACGGGTTCACCGGGCGCAGCAGCGTCTTCTGCCCTGCTGCACTGTGGCCGACCGGTG	2520
2452	DB	TA CGGGTTACGGGAGGGCAGCAGGACTCTCTGCCGTGCTGCACTGTCCCGGACGGTG	2511
2521	QY	ACGACCATCGCCCGCAGATGTCTCTCGGACGCGCGCGTACGTGACCGCGCTGGCGG	2580
2512	DB	ACGACCATCGCCCGCAGATGTGCTCGGACCGCGGAGTACGTCCACGCGGCTGGCGG	2571

Qy 2581 GAGTTCGATCAGCTGCGCCGACTTTCCGAGGCGCGGCATGCGGCGCCCGGTCG 2640
Db 2572 GCCTTCGACAGCTCCTCGCCGATTTCCGAGGCGCGGCATGCGGCGCCCGGCCC 2631
Qy 2641 TACTCCATGCGCATCATCTACGGGACACGAGACTCCATTTTCTGTTGTGCGCGGCTC 2700
Db 2632 TATTCATGCGCATCATCTACGGGACACGAGCTCCATATTTGTGCTGTGCGGCGCTC 2691
Qy 2701 ACGGCGCGGCGCTGTGTGCCATGCGGCGACAAGATGGCGAGCCACATCTCGCGCGCGTG 2760
Db 2692 ACGGCGCGGCGCTGTGCGCGCTGTGCGGCGACAAGATGGCGAGCCACATCTCGCGCGCGTG 2751
Qy 2761 TTCTCTCCCGCGATCAGCTGAGTGGCGAAGAAAGTTTCCAAAGCTGCTCTCATCGCC 2820
Db 2752 TTCTCTCCCGCGATCAAACTCGAGTGGCGAAGAGCTTCCAAAGCTGCTCTCATCGCC 2811
Qy 2821 AAGAAAAGTACATCGGCGTCACTGCGGGGCGAAGATGCTTCATCAAGGGCGTGGATCTG 2880
Db 2812 AAGAAAAGTACATCGGCGTCACTACGGGGTGAAGTCTCATCAAGGGCGTGAATCTG 2871
Qy 2881 GTGGCGAAAAACAATGCGCGTATTATCAACCGCACCTTCAGGGCGCTGTGTCGACTGCTG 2940
Db 2872 GTGGCGAAAAACAATGCGCGTATTATCAACCGCACCTTCAGGGCGCTGTGTCGACTGCTG 2931
Qy 2941 TTTTACGACGATACCGTATCGGAGCGCGCGCGTGTAGCGAGCGCCCGCAGAGGAG 3000
Db 2932 TTTTACGACGATACCGTATCGGAGCGCGCGCGTGTAGCGAGCGCCCGCAGAGGAG 2991
Qy 3001 TGGTGTGGCGGACCCCTGCGGAGGAGCTGCAGGCGTTTCGGGGCGCTCTCGTAGAGGCC 3060
Db 2992 TGGTGTGGCGGACCCCTGCGGAGGAGCTGCAGGCGTTTCGGGGCGCTCTCGTAGAGGCC 3051
Qy 3061 CATCGGCGCATACCGACCCGAGAGGAGCATTCAGAGACTTTTGTCTTCTCACCGCGAACTG 3120
Db 3052 CATCGGCGCATACCGACCCGAGAGGAGCATTCAGAGACTTTTGTCTTCTCACCGCGAACTG 3111
Qy 3121 AGCAGACACCGCGCGGTACCAACAAGCGCTTGGCCACCTGAGCGGTGTTATCAAG 3180
Db 3112 AGCAGACACCGCGCGGTACCAACAAGCGCTTGGCCACCTGAGCGGTGTTATCAAG 3171
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Db 3292 GCGCGCGCCAGGGAGCGCCGCCCGCCCGCGGCTGTGGCGCCCTTCGCGCCAGGCG 3351
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Qy 3481 ACGGACTATTACTTCTGCACTGCTGGGGGCGGCTGCGTGAGCTTCAAGGCGCTGTTT 3540
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Db 3592 CCCCGGAGACGCTGCGCGGCTCAGGGCGCGGGGTTTCGGGCGCGGTGGGTGCCGCG 3651

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RESULT 12
US-10-624-149A-1/c
; Sequence 1, Application US/10624149A
; Publication No. US20040109873A1
; GENERAL INFORMATION:
; APPLICANT: Neubauer, Antonie
; APPLICANT: Ziegler, Christina
; TITLE OF INVENTION: gm-Negative EHV-Mutants without Heterologous Elements
; FILE REFERENCE: 1/1372
; CURRENT APPLICATION NUMBER: US/10/624,149A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 60/403,282
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: DE 10233064
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: DE 10317008
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 1
; LENGTH: 150223
; TYPE: DNA
; ORGANISM: Equine herpesvirus 1
; PUBLICATION INFORMATION:
; AUTHORS: Telford, E.A.
; AUTHORS: Watson, M.S.
; AUTHORS: McBride, K.
; AUTHORS: Davison, A.J.
; TITLE: The DNA sequence of equine herpesvirus-1
; JOURNAL: Virology
; VOLUME: 189
; ISSUE: 1
; PAGES: 304-316
; DATE: JUL-1992
; DATABASE ACCESSION NUMBER: NC 001491, NCBI
; DATABASE ENTRY DATE: 2000-08-01
US-10-624-149A-1
Query Match 29,78; Score 1104.8; DB 19; Length 150223;
Best Local Similarity 59.18; Pred. No. 2e-271;
Matches 2131; Conservative 0; Mismatches 1317; Indels 156; Gaps 8;
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Db 54945 CCCACCAAGAGTGTACTGCGATGCTCAGAGTACGAGTGTGAACTTTGCTCTCGGAGG 54886
Qy 366 CTTCGCGCGCGTCTGCTTGGCGCTGTGGGGCGGTGCGGACCATGCCCCCAAGGGGTTCGA 425
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Db 54597 GGCAGAACTGTCGCGCAATGGTGAATGCGCGACAGCTCGGCTTTGAGCGCGCCT 54538
Qy 677 GCGAGGCTGCGCGGCGCTCGCGAGTCGCGGGGCGTCGTCGCG----- 728
Db 54537 GGGAAATGGCAACGCGCGCAACAGAGCGCGGACGCGGGGATGTCGGGCGGAAA 54478
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Qy 1446 GATCTACAAGTCCCGCTCGAGGCTACGGCGCATGAACGCGGGGTGTTCCGCT 1505
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Qy 1979 ----GGGAAGGGGAGCGCGCGGAGCGGAAACGCGGACGAGGATAAGGACGACGA 2033
Db 53217 AAGCCACGCTTCGACAGTACAGAGAACCGACGCTGTGACGCTACCCCGAGCGCGC 53158
Qy 2034 GGAAGAGA GCGGAGCGAGCGAGGAGTTCGCGCGAGACCGGGGCGCGCAGCTTGG 2093
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Qy 2094 GTACAGGGGCGCGGCTCTCGACCCCACTCGGGTTTCACTGCGACCGCGCTGGTGT 2153
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QY 2694 CGGCTCAGCGCCGGGCGCTGGCCATCGGCGACAAGATGGAGCCACATCTCGCG 2753
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QY 52437 GGACTCTTTAGAGCGCCCATCAAACTGGAGTGTGAGAAGACCTTTCAGCGACTGCTGCT 52378
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QY 52317 CGACTGGTCCGCAAAAATAACTGCTCTTTTCAATAACTTTGACGCGGACATCTGGTAGA 52258
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QY 52077 TGAGCTGAGCGCTCACCCGGAATCGTATACCAAGCGCTGCGCACCTCACCGTCTA 52018
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Db |||||
QY 51546 AGAA 51543
Db |||||
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RESULT 13
US-10-626-832-155
; Sequence 155, Application US/10626832
; Publication No. US2005000342A1
; GENERAL INFORMATION:
; APPLICANT: Davis Poynter, Nick
; APPLICANT: Nugent, Josephine
; APPLICANT: Birch-Machin, Ian
; APPLICANT: Allen, George P
; FILE OF INVENTION: Viral Marker
; TITLE REFERENCE: 620-262
; CURRENT APPLICATION NUMBER: US/10/626.832
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/398,576
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 155
; LENGTH: 3663
; TYPE: DNA
; ORGANISM: Equine herpesvirus 1
US-10-626-832-155
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Query Match 29.6%; Score 1100; DB 21; Length 3663;
Best Local Similarity 59.0%; Pred. No. 2e-270;
Matches 2128; Conservative 0; Mismatches 1320; Indels 156; Gaps 8;

QY 186 GGTTCAGCGGCATACGTACTACAGCGAGTGGCGAATTTGATTTATCGCCCCCGGTTTC 245
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QY 246 GCTGGAGGAGCGCCCGCGGAGCAGCACCAGCGGTCCACGCGCCGCTCCCGCG 305
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QY 306 CGCCCTTAAGGTGTAAGTTCGCGGGGGGACGAGCGGAGTCTCTCCCGTGGCGCGGAGG 365
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QY 486 CATCGCGCGCCCGCAGCTCCACGAGCGATTTATGGACGCCATCACGCCCGCGCGGACCGT 545
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QY 546 CATCAGCGTTCGGGTCTGAGCCCCCGAAGGCCATCGCGTTCGCGGTTCACGTCTACGGCAC 605
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QY 645 -----GCACCTCGAGTGCCTGCCCGCGC-----GATCTCT 676
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Db 53787 GCAACTAAACAAGAGCTTGGTAATTCAAATTTCTGTTGCTTTACTCTTTTAGCAACC 53728
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Qy 1573 GACATGTACGGCATCATCACCGACAGGTCAAACTCTCCAGCTACAAGCTGAACCGGTC 1632
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Qy 1633 GCCAGGGCGCTTTGAAGGACAAAGAGATCTGAGCTACCGGACATCCCGCCTAC 1692
Db 53307 GTTGAAGAGCTTCTAGGTGAGCAAGAATAGACCTTCCATACAAAGACATACCTTTTAC 53248
Qy 1693 TAGCCTCGGCCCGCGCGCGGGGTGATCGGGAGTATGTGTGAGAGACTCGCTG 1752
Db 53247 TATGCAAGTGGACCAACACAGCGGGGTGTAATAGGAGATATGTATTACGGACTCAAGA 53188
Qy 1753 CTGCTCGGGAGCTGTCTTCAAGTTTCTGCGCACCTTGAGCTTTCCGCGCTCGCGCG 1812
Db 53187 TTAGTTGGAAAGCTATTTTAAAGTACCTCCACATCTGGAACTCTGCTGTTGCAAG 53128
Qy 1813 CTGGCGGGATCAACATCACCGCACCATCTACGACGGCCAGCAGATCGGCTTCTACG 1872
Db 53127 CTAGCCCGCATAACTTAACGCGGGTAAATTTTGTGTTGTCAGCAAAATTCGGTTFACACA 53068
Qy 1873 TGCTCTCGGCTTTGCGGGCAGAGGGCTTCATCTCGCGGACACCCAGGGCGGTTT 1932
Db 53067 TGCTTGCTAAACTCGCCAGAGAGCGGAATTTTATTTTACCAAGCAACCGGCAAAATTC 53008
Qy 1933 CGGGGCTCGACAGGAGCGCCCAAGCGCCGCGCTGCTCGGGGGAGGGGAGCGG 1992
Db 53007 GACTACCATGGGAGCTGTGTGGAAGTTCCGAGACATCATATAATAGTGAAGACCAC 52948
Qy 1993 CGGGGGAGGGAAACGGGGAGAGGATAA-----GGACGACAGAGGAGGAGGACG 2044
Db 52947 GCCTTTGACAAACAATAACAATCAGATAGTATTAATGGAGCCAAAGATGTTATAGTCTG 52888
Qy 2045 GGGAGAGCGGAGAGGTGCGGCGCGAGACGGG-----GGCCGCACTTTGGGTACCAG 2100
Db 52887 TCTGCCATTTTGGAAACAGGGGGCGGAAACCCGGCAGAGTAGGATTTGTGGGATACCAA 52828
Qy 2101 GGGGCGCGGCTCTCGACCCCACTCCGGTTTACGTCGACCCCGTGTGTGTGTTTTCAC 2160
Db 52827 GGAGAAAGGTCTAGATCTTATATCCGGCTTTCATGTTGACCCAGTCTGTGTGTTTAC 52768
Qy 2161 TTGCGACCTGTATCCCGACATCATCCAGGCCCAACAACTGTGTCTCAGTACGCTCTCC 2220
Db 52767 TTGCGAGCTGTATCCCGACATCATCCAGGCCCAACAACTTTGTTTTCACCACTTAGCC 52708
Qy 2221 CTGGGCGCGAGGCGGTGCGGACCTTGAGGGGACCGGAGCTACTCGGAGATCGAGGTG 2280
Db 52707 CTTAATGAAGTGAATTTGGCTTTCAGCGGCTTTCAGCGGTGTGTGACTACTCAACGTTGAGGTG 52648

Qy 2281 GGGGCCCGACGGCTGTTCTTGTGAAGGCCACGTAACGAGAGCTGCTGAGCATCTCG 2340
Db 52647 GCGACAAAGTGTGTTTGTGTCAGCGGCACATTCGGGAAGCTTGTGTTGTTTGTG 52588
Qy 2341 CTGCGGATCTGGCTGGCATCGAAAGCAGATCCGCTCGCGGATCCCGCAGACACCC 2400
Db 52587 CTGCGGATCTGGCTGGCTATCGAAAGGCTGTAGGCGACGAATTCACAAAGTACCCG 52528
Qy 2401 GAGGAGGCGCTCTCTCTCGACNAGCAACAGGCGGCATCAAGGTGTGTGTCGAACTCGGTG 2460
Db 52527 GAGGAGGCGATTTTCTAGATAAGCAACAGTCTGCAATTTAAAGTAAATATGCAACTCAGTT 52468
Qy 2461 TACGGTTTACCGGGCGCAGCACGCTCTTCTGCGCTCTGCTGCACTGTGCGCCGCCACCGTG 2520
Db 52467 TACGGAITTCACGGTGTGGCAACCGACTGTGTGCCATGCTCTGAGNATAGCAGCCAGTT 52408
Qy 2521 ACGACCATCGCGCGGAGATGCTCTCGGACGCGCGGTACGTGCAACGCGCTGGCGG 2580
Db 52407 ACTCAATAGCGCGCAACATGCTTCTCAAAACGAGAGATTAAGTTTCACTATCGTTGGCG 52348
Qy 2581 GAGTTGATCAGCTGCTGGCGGACTTTTCGGAGGGCGCGGATCGCGCCCGCGCTCG 2640
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Qy 2641 TACTCCATCGGCATCATCTACGGGACACGGAATCTTCTGTTTGTGCGCGCGCTC 2700
Db 52287 TATCTGTGAGATTTTTCGGAGACACGACTCTGTATTCATCAAGTTTGTGGCTA 52228
Qy 2701 ACGCGCGCGGCTGTGTGCCATGCGGCGAAGATGGGAGCCACATCTCGCGCGCTG 2760
Db 52227 ACATACGAGGGGTTTTCAGAGCTTGGAGTTCAATGTGCGACAGATTTACGTGACCTT 52168
Qy 2761 TTCTTCCCGCGATCAAGCTCGAGTGCAGAAAGGTTTCAACAGCTGCTGCTCATCGC 2820
Db 52167 TTTAAGCACCTATCAAACTAGAGTGTGAAAAAACCTTTCCAGCGGCTGCTACTAATACA 52108
Qy 2821 AAGAAAAAGTACATCGCGCTCATCTCGGGGCGCAAGATGCTCATCAAGGCGGTGATCTG 2880
Db 52107 AAGAAAAAGTACATAGTGTATCAACGGGGGTATTAAGTCTCATGAGGGGTAGACCTA 52048
Qy 2881 GTGCGCAAAAACTGCGCTTTATCAACCGCACCTCCAGGGCGCTCGTTCGACCTGCTG 2940
Db 52047 GTCCGTAATAATACTGTGCTTATATAAATCTTACGCGGACATCTAGTAGATCTTCTG 51988
Qy 2941 TTTTACGAGGATACGTTATCGGAGCGCGCGCGGTTAGCGAGCGGCGCCCGCAGAGG 3000
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Qy 3001 TGGCTGGCGGACCCCTGCGGAGGAGCTGAGGGCTTTCGGGGCGCTCTCGTAGACGCG 3060
Db 51927 TGGGTTGGCGCGCCCTTCCGAGCGGCTTTCAGAGTTTGGNAGAGTGTGNTAGAGCT 51868
Qy 3061 CATCGGCGCATCAACGACCCCGAGAGGACATCCAGGACTTTGTCTTCCACCGCGAACTG 3120
Db 51867 TACAACGTAATAACCGCACCCAACTTGGATGTGCGGAGTTTGTGATGACGCTGAGCTT 51808
Qy 3121 AGCAGACACCCGCGGCTACACCAACGAGCGCTGCGGCCCACTGACCGTGTATTACAAG 3180
Db 51807 AGCCGACCGCGGAATCATATACAAACGAGGCTTACCGCACCTCACTGTTTACTTTAAG 51748
Qy 3181 CTCTAGCGCGCGCGGAGTCCCGTTCATCAAGGACCGGATCCCGTGTGATCTGCTG 3240
Db 51747 CTGCTATGCGGAATGAAGACTGCCCGAGTGTGAAGAGAGAAATTCGATGTGATGTTT 51688
Qy 3241 GCCCAGACCCCGAGGTAGAGGAGACGCTCGCGGGTGGCGCGCTCCCGGAGCTAGAC 3300
Db 51687 GCGCAAAACAGAAAGCGCTGAACGCGAAGCTTGTATAGTAAACTCCATCGCTG----- 51636
Qy 3301 GCCCGCGCCGAGGGGACGAGCCCGCCCCCGAGGGCGCTTCCCTCCCGCGCCAGCGC 3360
Db 51635 ----- 51636

Qy	3361	CCCCGGGAGACGCGTCGCATGCCGACCCCGGGAGCGCGTCCAAAGCCCCGCAAGCTG	3420
Db	51635	-----GTACTACAAACCCCGGCCATCAAAACACAAGCCCCCAATCCAAACGCAACTG	51580
Qy	3421	CTGGTGTCCGAGCTGGCGAGGATCCCGGGTACGGCTACGCCATCGCCCGGGCGTTCCGCTCAAC	3480
Db	51579	CTCGTTTCGGACCTGGCTGAGATCCAACTATGTTTCAGAAATGACGTTCCACTTAAC	51520
Qy	3481	ACGGACTATTACTTCTCGCACCTGCTGGGGCGGCGCTGCGTGACGTTCAAGGCCCTGTTT	3540
Db	51519	ACAGACTACTATTTTTCCACCTGTGGGTACGATAAGCGTAACCTTTAAGGCATTATTT	51460
Qy	3541	GGAAATACGCCAAGATCACCGAGAGTCTGTTAAAGGTTTATTCCCGAGACGTGGCAC	3600
Db	51459	GGAAATGATGCAAGACCCACAGAAACCTTTTAAAGCGATTATTTCAGAAAGACCCAC	51400
Qy	3601	---CCCCCGGACGAGTGGCGCGCGCTCAGGGCCGCGGGTTTCGGGCCCGCGGGGCC	3657
Db	51399	AAGACCTCCACAAAACCCAGGAGATGTTGGAGCGCGCTGGATTGAAAGGCTAACTCCC	51340
Qy	3658	GGCGCTACGGCGGAGGAAACTCGTCGAATGTTGCATAGAGCCTTTGATCTCTAGCA	3714
Db	51339	TTTACATCGCGGGAAGAAAGTCGTCGAATCTGCATACAGTTTGTGTACTCTAGAA	51283

Search completed: August 6, 2005, 15:33:30
Job time : 2235 secs

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OM nucleic - nucleic search, using sw model

Run on: August 5, 2005, 23:52:49 ; Search time 1860 Seconds

(without alignments)
11829.935 Million cell updates/sec

Title: US-10-692-556-1

Perfect score: 3717

Sequence: 1 atgtttgtgcgcggcggcggg.....cctttgatactctagcatga 3717

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001as.*

5: Geneseq2001bs.*

6: Geneseq2002as.*

7: Geneseq2002bs.*

8: Geneseq2003as.*

9: Geneseq2003bs.*

10: Geneseq2003cs.*

11: Geneseq2003ds.*

12: Geneseq2004as.*

13: Geneseq2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3717	100.0	3717	6 AAD30077	Aad30077 Herpes si
2	3696.2	99.4	3723	6 AAD30078	Aad30078 Herpes si
3	3696.2	99.4	14926	2 AAV62156	Aav62156 HSV-2 str
4	3696.2	99.4	117213	2 AAV62176	Aav62176 HSV-2 str
5	3693	99.4	154746	6 AAD25519	Aad25519 Human her
6	3059.8	82.3	3708	6 AAD30079	Aad30079 Herpes si
7	3053.4	82.1	3708	6 AAD30080	Aad30080 Herpes si
8	3047	82.0	3708	6 AAD30081	Aad30081 Herpes si
9	1104.8	29.7	149158	12 ADP74211	Adp74211 Equine he
10	1104.8	29.7	149261	12 ADP74212	Adp74212 Equine he
11	1104.8	29.7	150071	12 ADP74216	Adp74216 Equine he
12	1104.8	29.7	150223	12 ADP74201	Adp74201 Equine he
13	1100	29.6	3663	12 ADJ95524	Adj95524 Equine he
14	885.8	23.8	144411	12 ADP74214	Adp74214 Equine he
15	885.8	23.8	144486	12 ADP74215	Adp74215 Equine he
16	885.8	23.8	145444	12 ADP74213	Adp74213 Equine he
17	885.8	23.8	145596	12 ADP74202	Adp74202 Equine he
18	701.8	18.9	124884	5 AAH74201	Aah74201 Nucleotid
19	701.8	18.9	124884	10 ADA14878	Ada14878 Human her
20	701.8	18.9	124884	11 ADL99489	Adl99489 Varicella

c	21	697	18.8	125157	5	AAH74202	Aah74202 Nucleotid
	22	517.2	13.9	554	12	ADP82907	Adp82907 Human her
	23	515.4	13.9	558	12	ADP82906	Adp82906 Human her
	24	319.4	8.6	3048	2	AAT60714	Aat60714 DNA encod
c	25	319.4	8.6	172281	12	ADN12161	Adn12161 Epstein-B
	26	313.2	8.4	128139	6	AAI64291	Aai64291 RRV genom
	27	313.2	8.4	133719	3	AAC64754	Aac64754 Macaca mu
	28	243.6	6.6	2511	2	AAT51553	Aat51553 Herpes vi
	29	242	6.5	35100	2	AAV73802	Aav73802 KSHV LUR
	30	242	6.5	137507	2	AAV19941	Aav19941 KSHV long
	31	242	6.5	137508	12	ADN12162	Adn12162 Human her
	32	219	5.9	231	13	ADK51364	Adk51364 Herpesvir
	33	191.2	5.1	228	2	AAQ13715	Aaq13715 Sequence
	34	187	5.0	231	13	ADK51363	Adk51363 Herpesvir
	35	169.2	4.6	3729	6	AAD30082	Aad30082 Human cyt
	36	164.4	4.4	3729	13	ADR19896	Adr19896 HCMV AD16
c	37	164.4	4.4	229354	6	ABQ74179	Abq74179 Human cyt
	38	153.2	4.1	3039	2	AAQ91096	Aaq91096 Human her
	39	130	3.5	536	2	AAT51545	Aat51545 Herpes vi
	40	110.6	3.0	536	2	AAT51546	Aat51546 Herpes vi
	41	101.4	2.7	103	2	AAx31980	Aax31980 Sequence
	42	90.2	2.4	103	2	AAx31979	Aax31979 Sequence
	43	89	2.4	454	2	AAT51554	Aat51554 Herpes vi
	44	89	2.4	3435	2	AAT35869	Aat35869 Human DNA
	45	89	2.4	3443	5	AAS79309	Aas79309 DNA encod

ALIGNMENTS

RESULT 1

AAD30077

ID AAD30077 standard; DNA; 3717 BP.

XX AC AAD30077;

XX DT

17-MAY-2002 (first entry)

XX DE Herpes simplex virus (HSV2-MS-M1) mutant DNA polymerase gene.

XX KW Herpes virus; medicinal; therapy; binding domain; DNA polymerase gene;

XX KW antiviral; enzyme; mutant; ds.

XX OS Herpes simplex virus.

XX FH Key Location/Qualifiers

FT CDS 1..3717

FT /*tag= a

FT /product= "Mutant DNA polymerase"

XX PN W0200206513-A2.

XX PD 24-JAN-2002.

XX PF 13-JUL-2001; 2001WO-US016525.

XX PR 13-JUL-2000; 2000US-0218118P.

XX PR 13-APR-2001; 2001US-0283880P.

XX PA (PHAA) PHARMACIA & UPJOHN CO.

XX PI Homa FL, Wathen MW, Hopkins TA, Thomsen DR;

XX DR WPI; 2002-179800/23.

XX DR P-PSDB; AAE18853.

XX PT Selecting compounds that inhibit herpes viruses by comparing inhibitory concentration of a compound of interest that inhibits wild-type herpes virus and domain mutant herpes virus, and selecting compound of interest.

XX PS Claim 25; Fig 5; 126pp; English.

XX CC The present invention relates to a method for selecting compounds that

CC inhibit herpes viruses. The method involves measuring IC 5.0 of compound
 CC of interest that inhibits wild-type herpes virus and domain mutant herpes
 CC virus mutant herpes virus which is the same strain as wild-type herpes
 CC virus, comparing IC 5.0 of the compound inhibiting wild-type herpes virus
 CC with IC 5.0 of the compound inhibiting mutant herpes virus and selecting
 CC the compound, where IC 5.0 of the compound of interest that inhibits
 CC mutant herpes virus is at least 3 times greater than IC 5.0 of the
 CC compound that inhibits wild-type herpes virus. The method is useful for
 CC selecting compounds that inhibit herpes viruses. The compound is useful
 CC for manufacture of medicinals for selectively treating diseases caused by
 CC herpes viruses such as herpes viral infection, or for selectively
 CC inhibiting herpes viruses, in a human host by administering a compound to
 CC human in need of such treatment, where the compound inhibits herpes
 CC viruses by interaction with the binding domain in the viral DNA
 CC polymerase, and IC 5.0 of the compound that inhibits a binding domain
 CC mutant herpes virus is at least 3 times, preferably 5 times greater than
 CC IC 5.0 of the compound that inhibits the wild-type herpes virus which is
 CC the same strain as the mutant herpes virus. The present sequence is
 CC Herpes simplex virus (HSV2-MS-M1) mutant DNA polymerase gene
 XX
 SQ Sequence 3717 BP; 627 A; 1293 C; 1200 G; 597 T; 0 U; 0 Other;

Query Match 100.0%; Score 3717; DB 6; Length 3717;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTTTGTGCGGGGCGCGCGACTTCCCGGGGGGAAGTCGGGGCTCGGGGGCG 60
 Db 1 ATGTTTGTGCGGGGCGCGCGACTTCCCGGGGGGAAGTCGGGGCTCGGGGGCG 60
 Qy 61 TCTGGGTTTTTGGCCCCCAACACCCCGGGGAGCCACCCAGAGCGGACCGCGCTTGC 120
 Db 61 TCTGGGTTTTTGGCCCCCAACACCCCGGGGAGCCACCCAGAGCGGACCGCGCTTGC 120
 Qy 121 CGCGCGCAGAACTTCTAACAACCCCACTCGCTCAGACCGGAAACGCAAGGCCCC 180
 Db 121 CGCGCGCAGAACTTCTAACAACCCCACTCGCTCAGACCGGAAACGCAAGGCCCC 180
 Qy 181 GGGCGGCTCAGCGGCTAGCTACTACAGGAGTGGACGAAATTCGATTTATCGCCCG 240
 Db 181 GGGCGGCTCAGCGGCTAGCTACTACAGGAGTGGACGAAATTCGATTTATCGCCCG 240
 Qy 241 CGTTTCGTGACGAGGAGCGCCCGCGGAGCAGCGACCGGGGTCCACGACGCGCGCTC 300
 Db 241 CGTTTCGTGACGAGGAGCGCCCGCGGAGCAGCGACCGGGGTCCACGACGCGCGCTC 300
 Qy 301 CGGCGCCCTTAAGGTGTACTGCGGGGGGAGCGAGCGGACGTCCTCCGCTGGGCGCG 360
 Db 301 CGGCGCCCTTAAGGTGTACTGCGGGGGGAGCGAGCGGACGTCCTCCGCTGGGCGCG 360
 Qy 361 GAGGGCTTGGCGGCTCGCTTGGCGCTGTTGGGGCGGTGGGACATGCCCCAGGGG 420
 Db 361 GAGGGCTTGGCGGCTCGCTTGGCGCTGTTGGGGCGGTGGGACATGCCCCAGGGG 420
 Qy 421 TTGACCCCGACCGTCACCGTCTTCCAGTGTACGACATCTCGGAGCAGCTGGAAACGCG 480
 Db 421 TTGACCCCGACCGTCACCGTCTTCCAGTGTACGACATCTCGGAGCAGCTGGAAACGCG 480
 Qy 481 TACAGCATGCGCGCGCCAGCTCCACGAGCAATTTATGACGCCATCAAGCCCGCGGG 540
 Db 481 TACAGCATGCGCGCGCCAGCTCCACGAGCAATTTATGACGCCATCAAGCCCGCGGG 540
 Qy 541 ACCGTCATCAGCTTCTGGGTCTACCCCGGAAGGCCATCGCGTCCGCTTCAGTCTAC 600
 Db 541 ACCGTCATCAGCTTCTGGGTCTACCCCGGAAGGCCATCGCGTCCGCTTCAGTCTAC 600
 Qy 601 GGCACGCGGAGTACTTTTATCAACAAAGCGGAGGTGGATCGGCACCTGCACTGCGGT 660
 Db 601 GGCACGCGGAGTACTTTTATCAACAAAGCGGAGGTGGATCGGCACCTGCACTGCGGT 660
 Qy 661 GCCCGCGCGATCTCTGAGAGCGCTTGGCGGCGCCCTGCGGAGTGGCGGGGGCGTGC 720
 Db 661 GCCCGCGCGATCTCTGAGAGCGCTTGGCGGCGCCCTGCGGAGTGGCGGGGGCGTGC 720

Qy 721 TTCCGCGGATCTCCCGGACACACTTCGAGGCGGAGTGTGTGAGGCGCGCGCGCTGAC 780
 Db 721 TTCCGCGGATCTCCCGGACACACTTCGAGGCGGAGTGTGTGAGGCGCGCGCGCTGAC 780
 Qy 781 TATTACGAAACGCGCGCGCGCTGTACTACCGCGTCTTGTGTGAGAGCGGGCGCGCTG 840
 Db 781 TATTACGAAACGCGCGCGCGCTGTACTACCGCGTCTTGTGTGAGAGCGGGCGCGCTG 840
 Qy 841 GCTACTGTGCGAACAATTTTGCCTCGGATCAGGAAGTACGAGGGGGCGTTCGAGCC 900
 Db 841 GCTACTGTGCGAACAATTTTGCCTCGGATCAGGAAGTACGAGGGGGCGTTCGAGCC 900
 Qy 901 ACCACCGGTTTATCTGAGCAACCCCGGGTGTGTACCTTCGGCTGTGTTACCGCTCAAG 960
 Db 901 ACCACCGGTTTATCTGAGCAACCCCGGGTGTGTACCTTCGGCTGTGTTACCGCTCAAG 960
 Qy 961 CCGCGCGCGGAAACG 1020
 Db 961 CCGCGCGCGGAAACG 1020
 Qy 1021 GAGCTCGAGTTTAACTGCGAGCAACCTGCGCGTTCGAGGGGCGCATGTGTGACCTG 1080
 Db 1021 GAGCTCGAGTTTAACTGCGAGCAACCTGCGCGTTCGAGGGGCGCATGTGTGACCTG 1080
 Qy 1081 CCGCGCTTACAGCTCATGTGCTTCGATATCGAATGCAAGCGCGGGGGAGGACGAGCTG 1140
 Db 1081 CCGCGCTTACAGCTCATGTGCTTCGATATCGAATGCAAGCGCGGGGGAGGACGAGCTG 1140
 Qy 1141 GCCTTTCCGCTCGGAAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1200
 Db 1141 GCCTTTCCGCTCGGAAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1200
 Qy 1201 GACTGTCCACACCGCGCTCGAGCATCTCTCTGTTTCGCTCGGATCTCTCGGACCTC 1260
 Db 1201 GACTGTCCACACCGCGCTCGAGCATCTCTCTGTTTCGCTCGGATCTCTCGGACCTC 1260
 Qy 1261 CCGAGTCCCACTCAGCGATCTCGGCTCCAGGGGCTCGCGCGCGCGCGCGCTCGGAG 1320
 Db 1261 CCGAGTCCCACTCAGCGATCTCGGCTCCAGGGGCTCGCGCGCGCGCGCTCGGAG 1320
 Qy 1321 TTTGACGAGAAATTCGAGATGCTGCTGGCTTCATGACCTTCGTTCAAGCAGTACGGCCC 1380
 Db 1321 TTTGACGAGAAATTCGAGATGCTGCTGGCTTCATGACCTTCGTTCAAGCAGTACGGCCC 1380
 Qy 1381 GAGTTCGTGACGGGTACACATCATCACTTCGACTGCGCTTCGTTCCGTCGACCAAGCTG 1440
 Db 1381 GAGTTCGTGACGGGTACACATCATCACTTCGACTGCGCTTCGTTCCGTCGACCAAGCTG 1440
 Qy 1441 ACGGAGATCTACAAAGTCCCGCTCGACGGGTACGGGCGCATGAACGGCGCGGGTGTGTT 1500
 Db 1441 ACGGAGATCTACAAAGTCCCGCTCGACGGGTACGGGCGCATGAACGGCGCGGGTGTGTT 1500
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 Qy 1561 ATGTTGACATCAGCATGTAGGCATCATCACGCAAGGTCAAACTCTCCAGCTACAAG 1620
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 Qy 1621 CTGAAACCGCGCTCGCGAGCGCGCTTTTGAAGGACAAAGAGGATCTGAGCTACCGGAC 1680
 Db 1621 CTGAAACCGCGCTCGCGAGCGCGCTTTTGAAGGACAAAGAGGATCTGAGCTACCGGAC 1680
 Qy 1681 ATCCCGCTTACTACGCTTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1740
 Db 1681 ATCCCGCTTACTACGCTTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1740
 Qy 1741 CAGGATCTGCTGCTGCTGCGGAGCTTCTTCAAGTTTCTGCGCGACCTGAGCTTTC 1800
 Db 1741 CAGGATCTGCTGCTGCTGCGGAGCTTCTTCAAGTTTCTGCGCGACCTGAGCTTTC 1800

QY 1801 GCCGTCGCGCCTCGCGGCGATCAACATCAACCGCACCATCATCGACGCGCAGCAGATC 1860
DB 1801 GCCGTCGCGCCTCGCGGCGATCAACATCAACCGCACCATCATCGACGCGCAGCAGATC 1860
QY 1861 CGCGCTTCAGTGCCTCTCGGCTTCGCGGCGAAGAGGCTTCATCTCGCGGACACC 1920
DB 1861 CGCGCTTCAGTGCCTCTCGGCTTCGCGGCGAAGAGGCTTCATCTCGCGGACACC 1920
QY 1921 CAGGGCGGCTTCGCGGCGCTCGAACAGAGGCGCGCCAAAGCGCCCGGCGCTCGCGGG 1980
DB 1921 CAGGGCGGCTTCGCGGCGCTCGAACAGAGGCGCGCCAAAGCGCCCGGCGCTCGCGGG 1980
QY 1981 GAAGGGAGCGCGCGGGGACCGGAAACGCGGACGAGGATAGGACGACGAGGACGAG 2040
DB 1981 GAAGGGAGCGCGCGGGGACCGGAAACGCGGACGAGGATAGGACGACGAGGACGAG 2040
QY 2041 GACGGGACGAGCGGAGGAGGTGCGCGCGGAGACCGGGGCGCGGACGTTGGGTACGAG 2100
DB 2041 GACGGGACGAGCGGAGGAGGTGCGCGCGGAGACCGGGGCGCGGACGTTGGGTACGAG 2100
QY 2101 GGGGCGCGGCTTCGACCCACCTCCCGGCTTCACGTGCGACCCCGGTGTTGTTGAC 2160
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QY 2281 GGGGCGGACGCGCTGTTCTTCTGTAAGGCCACGCTAGCGAGAGCGTGTGAGCATCCTG 2340
DB 2281 GGGGCGGACGCGCTGTTCTTCTGTAAGGCCACGCTAGCGAGAGCGTGTGAGCATCCTG 2340
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QY 2461 TACGGGTTACCGGGGCGCAGACGGTCTTCTGCGCTGCGCTGACGTGGCGCCACCGTG 2520
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DB 2521 ACGACCATCGGCGCGAGATGCTCTCGCGACGCGCGGTACGTGACGCGCGCTGGGCG 2580
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DB 2581 GAGTTGATGAGCTGGCGGACCTTTCGAGAGCGGCGGCGATGCGGCGCCCGGCTCG 2640
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QY 2761 TTCTCTCCCGCATCAAGCTGAGTGGGAAAGAGTTCACCAAGCTGTGCTCATCGCC 2820
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QY 2821 AAGAAAAGTACATCGGCGTCTCTCGGGGCGAGATGCTCATCAAGGGGTGGATCTG 2880
DB 2821 AAGAAAAGTACATCGGCGTCTCTCGGGGCGAGATGCTCATCAAGGGGTGGATCTG 2880
QY 2881 GTGCGCAAAACAACTGCGCGTTTATCAACCGCACCTCCAGGGCGCTGTGACCTCTG 2940

DB 2881 GTGCGCAAAACAACTGCGCGTTTATCAACCGCACCTCCAGGGCGCTGTGTCAGCTGCTG 2940
QY 2941 TTTTACAGCATACCTGATCCGAGCGCGCGCGCTTAGCCGAGCGCCCGCAGAGAG 3000
DB 2941 TTTTACAGCATACCTGATCCGAGCGCGCGCGCTTAGCCGAGCGCCCGCAGAGAG 3000
QY 3001 TGGCTGCGGACCCCTGCGCGGAGGACTGCAAGCGCTTCGCGGCGCTCTCGTAGACGC 3060
DB 3001 TGGCTGCGGACCCCTGCGCGGAGGACTGCAAGCGCTTCGCGGCGCTCTCGTAGACGC 3060
QY 3061 CATCGGCGCATCAACCGACCCCGAGGAGCAATCCAGGACTTTGTCTTCTCACCGCGAACTG 3120
DB 3061 CATCGGCGCATCAACCGACCCCGAGGAGCAATCCAGGACTTTGTCTTCTCACCGCGAACTG 3120
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DB 3121 AGCAGACACCGCGCGGTACCAACAAAGCGCTGCGCCACCTGACGGTGTATTACAG 3180
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QY 3301 GCCCGCGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3360
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DB 3361 CCCCGGAGACGCGCTGCGCATGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 3420
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DB 3421 CTGCTGTCCGAGTGGCGGAGATCCCGGTTACGCCATCGCGCGCGCGCGCGCGCG 3480
QY 3481 ACGGACTTATTCTTCTGCGACCTGCTGGGCGCGCGCTGCGTAGCTTCAAGGCCCTGTT 3540
DB 3481 ACGGACTTATTCTTCTGCGACCTGCTGGGCGCGCGCTGCGTAGCTTCAAGGCCCTGTT 3540
QY 3541 GGAATAAAGCCCAAGATCACCGAGAGTCTGTTAAAGAGGTTTATTCGCCGAGACGTGGC 3600
DB 3541 GGAATAAAGCCCAAGATCACCGAGAGTCTGTTAAAGAGGTTTATTCGCCGAGACGTGGC 3600
QY 3601 CCCCGGACGACGTGGCGCGCGCTCAGGGCGCGGGTTTCGGGCGCGGGCGCGCGCG 3660
DB 3601 CCCCGGACGACGTGGCGCGCGCTCAGGGCGCGGGTTTCGGGCGCGGGCGCGCGCG 3660
QY 3661 GCTACGCGGAGGAACTCGTGCATGTTGCATAGAGCTTGTGATCTAGCATGA 3717
DB 3661 GCTACGCGGAGGAACTCGTGCATGTTGCATAGAGCTTGTGATCTAGCATGA 3717

RESULT 2

AAD30078
ID AAD30078 standard; DNA; 3723 BP.

XX AAD30078;

XX 17-MAY-2002 (first entry)

XX Herpes simplex virus (HSV2-186-M1) mutant DNA polymerase gene.

XX Herpes virus; medicinal; therapy; binding domain; DNA polymerase gene;

XX antiviral; enzyme; mutant; ds.

XX Herpes simplex virus.

Key Location/Qualifiers
FH 1. .3723
CDS

/*tag= a
/product= "Mutant DNA polymerase"

WO200206513-A2.

24-JAN-2002.

13-JUL-2001; 2001WO-US016525.

13-JUL-2000; 2000US-0218118P.

13-APR-2001; 2001US-0283880P.

(PHAA) PHARMACIA & UPJOHN CO.

Homa FL, Wathen MW, Hopkins TA, Thomsen DR;

WPI; 2002-179800/23.

P-PSDB; AAE18854.

Selecting compounds that inhibit herpes viruses by comparing inhibitory concentration of a compound of interest that inhibits wild-type herpes virus and domain mutant herpes virus, and selecting compound of interest.

Claim 25; Fig 5; 126pp; English.

The present invention relates to a method for selecting compounds that inhibit herpes viruses. The method involves measuring IC₅₀ of compound of interest that inhibits wild-type herpes virus and domain mutant herpes virus mutant herpes virus which is the same strain as wild-type herpes virus, comparing IC₅₀ of the compound inhibiting wild-type herpes virus with IC₅₀ of the compound inhibiting mutant herpes virus and selecting the compound, where IC₅₀ of the compound of interest that inhibits mutant herpes virus is at least 3 times greater than IC₅₀ of the compound that inhibits wild-type herpes virus. The method is useful for selecting compounds that inhibit herpes viruses. The compound is useful for manufacture of medicinals for selectively treating diseases caused by herpes viruses such as herpes viral infection, or for selectively inhibiting herpes viruses, in a human host by administering a compound to human in need of such treatment, where the compound inhibits herpes viruses by interaction with the binding domain in the viral DNA polymerase, and IC₅₀ of the compound that inhibits a binding domain mutant herpes virus is at least 3 times, preferably 5 times greater than IC₅₀ of the compound that inhibits the wild-type herpes virus which is the same strain as the mutant herpes virus. The present sequence is Herpes simplex virus (HSV2-186-M1) mutant DNA polymerase gene

Sequence 3723 BP; 625 A; 1295 C; 1206 G; 597 T; 0 U; 0 Other;

Query Match 99.4%; Score 3696.2; DB 6; Length 3723;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 3714; Conservative 0; Mismatches 3; Indels 6; Gaps 1;

Qy 1 ATGTTTGTGCGGGGGGGCCGACCTTCCCGGGGGGAGTCCGGCGCTCGGGCGGCG 60

Db 1 ATGTTTGTGCGGGGGGGCGCGGCTTCCCGGGGGGAGTCCGGCGCTCGGGCGGCG 60

Qy 61 TCTGGGTTTTTGGCCCCCAACCCCGGGGAGCCACCCAGAGCGCACCGCGCCCTTGC 120

Db 61 TCTGGGTTTTTGGCCCCCAACCCCGGGGAGCCACCCAGAGCGCACCGCGCCCTTGC 120

Qy 121 CGCCGGCAGAACTTTTAAACCCCCACCTCGCTCAGACCGGAAACGAGCCCAAGGCCCC 180

Db 121 CGCCGGCAGAACTTTTAAACCCCCACCTCGCTCAGACCGGAAACGAGCCCAAGGCCCC 180

Qy 181 GGGCGGCTCAGCGGCATAGTACTACGAGGTGCGAGCAATTTTCGATTTATCGCCCG 240

Db 181 GGGCGGCTCAGCGGCATAGTACTACGAGGTGCGAGCAATTTTCGATTTATCGCCCG 240

Qy 241 CGTTTCGTGACGAGGAGCGCCCCCGGAGCAGCGCACCGGGTCCACGACGGCGGCTC 300

Db 241 CGTTTCGTGACGAGGAGCGCCCCCGGAGCAGCGCACCGGGTCCACGACGGCGGCTC 300

Qy 301 CGGCGCGCCCTAAGGTGTACTCGGGGGGACGAGCGGACGTCTCCGGGTGGGCGCG 360

Db 301 CGGCGCGCCCTAAGGTGTACTCGGGGGGACGAGCGCACGTCTCTCGGTGGGCGCG 360

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Db 361 GAGGGCTTCTGGCGCGGCTCGCTTGGCGCTGTGGGGGGTGGGACCATGCCCAAGGGG 420

Qy 421 TTGACCCCCACCGTCAACCGCTCTTCCAGCTGTACGACATCTTGAGACGACGTGGAAACGCG 480

Db 421 TTGACCCCCACCGTCAACCGCTCTTCCAGCTGTACGACATCTTGAGACGACGTGGAAACGCG 480

Qy 481 TACAGCATGCGCGCGCCAGCTCCAGAGCATTTATGACGCCCATACGCGCGCGGG 540

Db 481 TACAGCATGCGCGCGCCAGCTCCAGAGCATTTATGACGCCCATACGCGCGCGGG 540

Qy 541 ACCGTCAATCAGCTTCTGGGTCTGAGCCCCGAAAGGCCATCGCTCGCGCTTACGCTAC 600

Db 541 ACCGTCAATCAGCTTCTGGGTCTGAGCCCCGAAAGGCCATCGCTCGCGCTTACGCTAC 600

Qy 601 GGCACGCGCAGTACTTTTACATGAACAAGCGGAGGTGGATCGGCACCTGCACTGCGCT 660

Db 601 GGCACGCGCAGTACTTTTACATGAACAAGCGGAGGTGGATCGGCACCTGCACTGCGCT 660

Qy 661 GCCCGCGCGCATCTCGCGAGCGCTGCGCGCGCGCTTGCAGTGC CGCGGGCGTGC 720

Db 661 GCCCGCGCGCATCTCGCGAGCGCTTGGCGCGCGCGCTTGCAGTGC CGCGGGCGTGC 720

Qy 721 TTCGGGGCATCTCCGCGGACCACTTTCGAGGCGGAGGTGTGAGCGCGCGCGACGTGATC 780

Db 721 TTCGGGGCATCTCCGCGGACCACTTTCGAGGCGGAGGTGTGAGCGCGCGCGACGTGATC 780

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Db 781 TATTAGAAACGCGCGCGACCCCTGTAACCGCGCTCTTCTGTGCGAAGCGGGCGCGCGCTG 840

Qy 841 GCCTACTGTGCGACAACTTTTCCCGCGCATCAGAAAGTACAGAGGGGGCGTGCAGCGCC 900

Db 841 GCCTACTGTGCGACAACTTTTCCCGCGCATCAGAAAGTACAGAGGGGGCGTGCAGCGCC 900

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Db 901 ACCACCGGTTTTATCTGGAACACCGGGGTGTGACCTTTCGGTGTGTTACCGCTCAAG 960

Qy 961 CCGCGCGCGGGAAACGCGCGCGCCCAACCGCGCGCCCGCGCGCTTCCGAACTCGAGC 1020

Db 961 CCGCGCGCGGGAAACGCGCGCGCCCAACCGCGCGCCCGCGCGCTTCCGAACTCGAGC 1020

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Qy 1201 GACGTGCAACACCGGCTTCGAGACATCTCTGTGTTTCGCTCGGATCTCTGAGCTC 1260

Db 1201 GACGTGCAACACCGGCTTCGAGACATCTCTGTGTTTCGCTCGGATCTCTGAGCTC 1260

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Db 1261 CCGAGTTCACCTCAGCGATCTCGCTCCAGGGGCTCGCGGCCCGCGCTCGTCTGGAG 1320

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Qy 1381 GAGTTCGTGACCGGGTACACATCATCACTTCGACTGGCCCTTCGCTTCGACCAAGCTG 1440

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Db 1801 GCCGTGCGCGCTCGGCGGCATCAACATCAACCGCACCATCTACGACGCGCCAGCATC 1860
Qy 1861 CGCGTCTTACGTCCTCTCGGCTTCGCGGCCAGAAAGGCTTCATCTGCGCGACACC 1920
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QY 3715 TGA 3717
D 3721 TGA 3723

RESULT 3
AAV62156
ID AAV62156 standard; DNA; 14926 BP.
XX
AC AAV62156;
AC AAV62156;
DT 18-DEC-1998 (first entry)
XX
DE HSV-2 strain SB5 Contig ID 12 DNA sequence.
XX
KW HSV-2 strain SB5; immunological response induction; therapy;
KW antiviral identification; viral protein inhibitor; ss.
XX
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XX
FH Key Location/Qualifiers
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XX WO9820016-A1.
XX 14-MAY-1998.
XX
XX 31-OCT-1997; 97WO-US020016.
XX
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PR 04-NOV-1996; 96US-0030279P.
PR 09-JUN-1997; 97US-0049018P.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Esser KM, Chan JY, Dabrowski-Amaral CE, Delvecchio AM, Dillon SB;
XX Leary JJ;
XX
XX WPI; 1998-286847/25.
XX
XX P-PSDB; AAW72104, AAW72105, AAW72106, AAW72107, AAW72108, AAW72109,
XX AAW72110, AAW72111.
XX
XX Herpes simplex virus type-2 sequences - useful in, e.g. prevention and
XX treatment of infection or inducing immunological response in mammal.
XX
XX Claim 1; Page 383-389; 748pp; English.
XX
XX This sequence represents a Herpes simplex virus type-2 (HSV-2) DNA
XX sequence of the invention. This sequence was isolated from HSV-2 strain
XX SB5 (deposited as ATCC VR-2546), is designated Contig ID 12, and encodes
XX 8 HSV-2 proteins. The proteins can be used for the treatment or
XX prevention of disease, to induce an immunological response in a mammal or
XX to identify inhibitors, activators or novel antivirals. Antagonists of
XX the proteins can be used to inhibit a viral polypeptide. The DNA sequence
XX or a vector containing it can also be used to induce an immunological
XX response in a mammal
XX
XX Sequence 14926 BP; 2332 A; 5133 C; 5177 G; 2284 T; 0 U; 0 Other;
XX
XX Query Match 99.4%; Score 3696.2; DB 2; Length 14926;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 3714; Conservative 0; Mismatches 3; Indels 6; Gaps 1;
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D 6750 TACAGCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6809
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D 6810 ACCGTATACAGCTTCTGGGTCTGAGCCCCCGAGAGGCCATCGCGTTCGCGCTAC 6869
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DB 7230 CCCGCGCGGGAACGCGCCCGGCCCAACCGCGCCCGCCGACGCGGTTTCGGAACTTCGAGC 7289
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QY 1381 GAGTTCTGACCGGGTACACATCATCAACTTCGACTGGCCCTTCGCTCGACCAAGCTG 1440
DB 7650 GAGTTCTGACCGGGTACACATCATCAACTTCGACTGGCCCTTCGCTCGACCAAGCTG 7709
QY 1441 ACGGAGATCTACAAGTCTCCGCTCGACGGGTACCGGCGCATGAACGCGGGGTGCTTC 1500
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QY 1501 CGCGTGGGACATCGCGCAGAGCCACTTTCAGAAAGCGACGAAGATCAAGGTGAACGGG 1560
DB 7770 CGCGTGGGACATCGCGCAGAGCCACTTTCAGAAAGCGACGAAGATCAAGGTGAACGGG 7829
QY 1561 ATGCTGAACATCGACATGATAGGATCATCAACGACAGGTCAAACTCTCCAGTACAAG 1620
DB 7830 ATGCTGAACATCGACATGATAGGATCATCAACGACAGGTCAAACTCTCCAGTACAAG 7889
QY 1621 CTGAACCGCGTCGCGCGGCGCTCTTGAAGGACGAAGAGGATCTGAGTACCGGAC 1680
DB 7890 CTGAACCGCGTCGCGCGGCGCTCTTGAAGGACGAAGAGGATCTGAGTACCGGAC 7949
QY 1681 ATCCCCGCTACTACGCTTCGCGGCCCGCGAGCGCGGGGTGATTCGCGGAGTATTGTGTG 1740

DB 7950 ATCCCCGCTACTACGCTTCGCGGCCCGCGAGCGCGGGTGAATCGCGGAGTATTGTGTG 8009
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Qy 3715 TGA 3717

Db 9990 TGA 9992

RESULT 4
AAV62176
ID AAV62176 standard; DNA; 117213 BP.
XX AC AAV62176;
XX

13-JAN-1999 (first entry)

XX HSV-2 strain SB5 Contig ID 15 DNA sequence.

DE HSV-2 strain SB5; immunological response induction; therapy;

XX antiviral identification; viral protein inhibitor; ss.

KW Herpes simplex virus 2.

OS

XX

PH Location/Qualifiers

CDS 755..1297

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FT /note= "encoded protein shown in AAW72170"

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FT /note= "encoded protein shown in AAW72245"

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FT /*tag= n

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FT /note= "encoded protein shown in AAW72176"

FT complement(11905..14520)

FT /*tag= p

FT /product= "ORF#9a protein"

FT /note= "encoded protein shown in AAW72223"

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D	b	54693	CGGGCGCCCTTAAGGTGTAAGTGGGGGAGCGAGCGCAAGCTCTCTCGCGTGGGCCG	54752	Q	y	1441	ACGGAGATCTACAAGGTCCCGCTCGACGGGTACGGGCGCATGAACCGCGGGGTGTGTTT	1500
Q	y	361	GAGGGCTTCTGGCGCGCTCGCTTGGCGCTGTGGGGGGTGGGACCATGATGCCCAAGGGG	420	D	b	55833	ACGGAGATCTACAAGGTCCCGCTCGACGGGTACGGGCGCATGAACCGCGGGGTGTGTTT	55892
D	b	54753	GAGGGCTTCTGGCGCGCTCGCTTGGCGCTGTGGGGGGTGGGACCATGATGCCCGAGGGG	54812	Q	y	1501	CGGCTGTGGGACATCGGCGCAGAGCCACTTTTCAGAACGCGCAGCAAGATCAAGTGAACGG	1560
Q	y	421	TTGACCCCAACGCTACCGTCTTCCAGTGTACAGATCTCTGAGCACTGTGGAACACGCG	480	D	b	55893	CGGCTGTGGGACATCGGCGCAGAGCCACTTTTCAGAACGCGCAGCAAGATCAAGTGAACGG	55952
D	b	54813	TTGACCCCAACGCTACCGTCTTCCAGTGTACAGATCTCTGAGCACTGTGGAACACGCG	54872	Q	y	1561	ATGGTCAACATGACATGTAGCGCATCATCACGACAAAGTCAAACTCTCCAGCTACAAG	1620
Q	y	481	TACAGATCGCGCGCCAGCTCCAGAGCGGATTTATGACGCCATCAGCCCGCGGG	540	D	b	55953	ATGGTCAACATGACATGTAGCGCATCATCACGACAAAGTCAAACTCTCCAGCTACAAG	56012
D	b	54873	TACAGATCGCGCGCCAGCTCCAGAGCGGATTTATGACGCCATCAGCCCGCGGG	54932	Q	y	1621	CTGAACGCCGTCCCGAGGCCGTCTTGAAGGACAAGAAAGGATCTGAGCTACCCGAC	1680
Q	y	541	ACGCTCATACGCTTCTGGGTCTGACCCCGAAGGCCATCGCGTGGCGCTTCAAGCTCTAC	600	D	b	56013	CTGAACGCCGTCCCGAGGCCGTCTTGAAGGACAAGAAAGGATCTGAGCTACCCGAC	56072
D	b	54933	ACGCTCATACGCTTCTGGGTCTGACCCCGAAGGCCATCGCGTGGCGCTTCAAGCTCTAC	54992	Q	y	1681	ATCCCGCGCTACTACGCCCTCGGGCCCGCAGCGCGGGGTGATCGGCGAGTATTGTG	1740
Q	y	601	GGCAGCGGAGTACTTTTATGAAACAAAGCGGAGGTGATCGGCACTTGCAGTGCCTG	660	D	b	56073	ATCCCGCGCTACTACGCCCTCGGGCCCGCAGCGCGGGGTGATCGGCGAGTATTGTG	56132
D	b	54993	GGCAGCGGAGTACTTTTATGAAACAAAGCGGAGGTGATCGGCACTTGCAGTGCCTG	55052	Q	y	1741	CAGGACTCGCTGCTGTCGGGCGAGCTTCTTCAAGTCTTTCGCGCACCTGGAGCTTTCC	1800
Q	y	661	GCCCGCGCATCTCTCGAGCGCTGGCGCGCCCTGCGAGTGCAGCGGGGGGTG	720	D	b	56133	CAGGACTCGCTGCTGTCGGGCGAGCTTCTTCAAGTCTTTCGCGCACCTGGAGCTTTCC	56192
D	b	55053	GCCCGCGCATCTCTCGAGCGCTGGCGCGCCCTGCGAGTGCAGCGGGGGGTG	55112	Q	y	1801	GCGCTCGCGCTCGCGGCGCATCAACATCACCGCACCATCTAACAAGCGCCAGAGATC	1860
Q	y	721	TTCCGGCGCATCTCCGGGACCACTTCAGGCGGAGGTGAGCGCGCGGACGCTGATC	780	D	b	56193	GCGCTCGCGCTCGCGGCGCATCAACATCACCGCACCATCTAACAAGCGCCAGAGATC	56252
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D	b	55173	TATTAAGAAACGGCGCCGACCTGTACTACCGGTCTTCTGTGGAAGCGGCGCGCTG	55232	Q	y	1921	CAGGGCGGTTTCGGGGCTTCGACAAAGAGGCGCCCAAGCGCGCGCGCTGCTCGGGG	1980
Q	y	841	GCTTACCTGCGGACAACTTTTCCCGCGCATCAGGAAGTACGAGGGGGCGTCAAGCC	900	D	b	56313	CAGGGCGGTTTCGGGGCTTCGACAAAGAGGCGCCCAAGCGCGCGCTGCTCGGGG	56372
D	b	55233	GCTTACCTGCGGACAACTTTTCCCGCGCATCAGGAAGTACGAGGGGGCGTCAAGCC	55292	Q	y	1981	GAAGGGAGCGGCGCGGGGACGGGAAACGGGAGCGAGGATAAGGACGACGACGA	2034
Q	y	901	ACCACCGGTTTATCTGGAACACCGGGGTTTGTACCTTTCGGCTGGTACCGCTCAAG	960	D	b	56373	GAAGGGAGCGGCGCGGGGACGGGAAACGGGAGCGAGGATAAGGACGACGACGACGA	56432
D	b	55293	ACCACCGGTTTATCTGGAACACCGGGGTTTGTACCTTTCGGCTGGTACCGCTCAAG	55352	Q	y	2035	GACGAGCGGGAGCAGCGCGCAGAGGAGTCCGCGCGAGACCGGGGGCGGACGTTGGG	2094
Q	y	961	CCGCGCGCGGAAACGGCGCGGCGCAACCGCGCGCCCGCGAGCGGTTTCGAACTCGAGC	1020	D	b	56433	GACGAGCGGGAGCAGCGCGCAGGAGGTTCCGCGCGAGACCGGGGGCGGACGTTGGG	56492
D	b	55353	CCGCGCGCGGAAACGGCGCGGCGCAACCGCGCGCCCGCGAGCGGTTTCGGAACCTCGAGC	55412	Q	y	2095	TACACGGGGCGCGGGTCTCTCGACCCCACTCCGGGTTCACGTCGACCCCGCTGGTGGTG	2154
Q	y	1021	GAGTCTGAGTTTAAGTCAAGCGGCAACCTGCGCTCGAGGGGGCATGTGTACCTG	1080	D	b	56493	TACACGGGGCGCGGGTCTCTCGACCCCACTCCGGGTTCACGTCGACCCCGCTGGTGGTG	56552
D	b	55413	GAGTCTGAGTTTAAGTCAAGCGGCAACCTGCGCTCGAGGGGGCATGTGTACCTG	55472	Q	y	2155	TTTGAATTTGCCAGCTGTACCCAGCATCATCCAGGCCCAAACTGTGTCTTCAATGACG	2214
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D	b	55473	CCGGCTTCAAGCTCATGTGCTTCGATATCGAATGCAAGCCCGGGGGGAGGACGAGCTG	55532	Q	y	2215	CTCTCCTCGGGCCGAGCGCGTCCGCACTTGGAGCGGACCGGGACTACCTTGGAGATC	2274
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D	b	55533	GCCTTTCGGTCCGGGAAACGCCCGGAGAGCTCTGTCATTCAGATCTCTGTCTGTCTAC	55592	Q	y	2275	GAGTGGGGGGCGAGCGGGTGTCTTCTGTAAGGCCCAAGTACGCGAGAGCTCTGTGAGC	2334
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D	b	55593	GACTGTCCACACCGCTCTGAGCAGATCTCTGTCTTTCGCTCGATCTCTCGACCTC	55652	Q	y	2335	ATCCTGCTGCGACCTGGCTGGCCATCGGAAAGCAGATCGGCTCGGGATCCCGCAGAGC	2394
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D	b	55653	CCGAGTCCCACTCAGCGATCTGCTCTCAGGGGCTGCGGCGCCCGCTGCTCTGAGAG	55712	Q	y	2395	ACCCCGAGGAGCGCTCTCTCTCGACAAAGCAAGCGCGCCCATCAAGGTGGTGTCAAC	2454
Q	y	1321	TTTGAAGAGCAATTCAGAGTCTGCTGCTTCTGATGACCTTCTGATGAGTACGAGCC	1380	D	b	56793	ACCCCGAGGAGCGCTCTCTCTCGACAAAGCAAGCGCGCCCATCAAGGTGGTGTCAAC	56852
D	b	55713	TTTGAAGAGCAATTCAGAGTCTGCTGCTTCTGATGACCTTCTGATGAGTACGAGCC	55772					

CC	the invention
XX	
SQ	Sequence 154746 BP; 23003 A; 54218 C; 54701 G; 22824 T; 0 U; 0 Other;
	Query Match 99.4%; Score 3693; DB 6; Length 154746; Best Local Similarity 99.7%; Pred. No. 0; Matches 3712; Conservative 0; Mismatches 5; Indels 6; Gaps 1;
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QY	961 CCCGGCGCGGGAACGCGCGGCCCAACCGCGCCCCCGACGCGGCTTCGGAACCTCGAGC 1020

PI Homa FL, Wathen MW, Hopkins TA, Thomsen DR;
XX
XX WPI; 2002-179800/23.
XX P-PSDB; AAE18855.
XX
XX Selecting compounds that inhibit herpes viruses by comparing inhibitory
PT concentration of a compound of interest that inhibits wild-type herpes
PT virus and domain mutant herpes virus, and selecting compound of interest.
XX
XX Claim 25; Fig 5; 126pp; English.
XX
XX The present invention relates to a method for selecting compounds that
CC inhibit herpes viruses. The method involves measuring IC₅₀ of compound
CC of interest that inhibits wild-type herpes virus and domain mutant herpes
CC virus mutant herpes virus which is the same strain as wild-type herpes
CC virus, comparing IC₅₀ of the compound inhibiting wild-type herpes virus
CC with IC₅₀ of the compound inhibiting mutant herpes virus and selecting
CC the compound, where IC₅₀ of the compound of interest that inhibits
CC mutant herpes virus is at least 3 times greater than IC₅₀ of the
CC compound that inhibits wild-type herpes virus. The method is useful for
CC selecting compounds that inhibit herpes viruses. The compound is useful
CC for manufacture of medicinals for selectively treating diseases caused by
CC herpes viruses such as herpes viral infection, or for selectively
CC inhibiting herpes viruses, in a human host by administering a compound to
CC human in need of such treatment, where the compound inhibits herpes
CC viruses by interaction with the binding domain in the viral DNA
CC polymerase, and IC₅₀ of the compound that inhibits a binding domain
CC mutant herpes virus is at least 3 times, preferably 5 times greater than
CC IC₅₀ of the compound that inhibits the wild-type herpes virus which is
CC the same strain as the mutant herpes virus. The present sequence is
CC Herpes simplex virus (HSV1-KOS-M1) mutant DNA polymerase gene
XX
XX Sequence 3708 BP; 662 A; 1236 C; 1200 G; 610 T; 0 U; 0 Other;
SQ

Query Match 82.3%; Score 3059.8; DB 6; Length 3708;
Best Local Similarity 89.3%; Pred. No. 0;
Matches 3321; Conservative 0; Mismatches 387; Indels 9; Gaps 2

QY	541	ACCGTCA	TCA	CGGTTCT	GGGTC	TGAC	CCCCCG	GAAGGCC	ATCG	CGT	CGCCG	TTCA	CGCTCT	AC	600
DB	538	ACCGTCA	TCA	CGGTTCT	GGGTC	TGAC	CCCCCG	GAAGGCC	ATCG	CGT	CGCCG	TTCA	CGCTCT	AC	597
QY	601	GGCAGC	GGC	GAGTACT	TTTAC	ATGA	CAAGG	CGGAGG	TGGAT	CGG	CAC	CTG	CAGT	GCCGT	660
DB	598	GGCAGC	GGC	GAGTACT	TTTAC	ATGA	CAAGG	CGGAGG	TGGAT	CGG	CAC	CTG	CAGT	GCCGT	657
QY	661	GCCCCG	CGG	ATCT	CTG	CAG	AGCC	TGCG	GGGGCC	TGCG	CGAG	T	CGCGGGG	CGT	720
DB	658	GCCCCA	CAG	ATCT	CTG	CAG	AGCC	TGCG	GGGGCC	TGCG	CGAG	T	CGCGGGG	CGT	717
QY	721	TTCCGG	GGG	CATCT	CTCCG	GAC	ACA	CTTC	GAG	GGCG	GAGT	TGGT	GGAG	GGCGCC	780
DB	718	TTCCGG	GGG	CATCT	CTCCG	GAC	ACA	CTTC	GAG	GGCG	GAGT	TGGT	GGAG	GGCGCC	777
QY	781	TATTAG	AAAC	GGCCG	CCG	ACTT	G	TACT	AC	CGCG	CTT	CTG	TG	CGAAG	840
DB	778	TACTAG	AAAC	GGCCG	CCG	ACTT	G	TATT	AC	CGCG	CTT	CTG	TG	CGAAG	837
QY	841	GCCTAC	CTG	TG	GAC	AACTTT	TG	CCCCG	CGAT	CAG	GAAT	GA	AGGGGG	CGG	900
DB	838	TGCTAC	CTG	TG	GAC	AACTTT	TG	CCCCG	CGAT	CAG	GAAT	GA	AGGGGG	CGG	897
QY	901	ACAC	CCGG	TTTAT	CTCTG	ACA	CAAC	CCGGGG	TTTGT	CAC	CTT	CGG	CTGG	TAC	960
DB	898	ACCAC	CCGG	TTAT	CTCTG	ACA	CAAC	CCGGGG	TTTGT	CAC	CTT	CGG	CTGG	TAC	957
QY	961	CCGGCG	CGG	GAA	CGCG	CGG	CCCA	ACCG	CGCCCC	CCCG	ACCG	CGCG	TTTCGG	AAAC	1020
DB	958	CCGGCG	CGG	AA	CAAC	ACG	TGAC	CGCC	AGCG	GGCCCC	CCG	ATGG	CC	T	1017
QY	1021	GACGT	CGAG	TTTAA	CTG	CA	CGCG	GAA	CAACT	TG	CGCG	T	CGAGGG	GCG	1080
DB	1018	GACGT	CGAG	TTTAA	CTG	CA	CGCG	GAA	CAACT	TG	CGCG	T	CGAGGG	GCG	1077
QY	1081	CCGGCC	TAC	AGCT	CAT	GTG	CTTC	GAT	ATCG	AATG	CAAG	CGCGGG	GAGG	ACG	1140
DB	1078	CCGGCA	TAC	AGCT	CAT	GTG	CTTC	GAT	ATCG	AATG	CAAG	CGCGGG	GAGG	ACG	1137
QY	1141	GCCTTT	CCGG	T	CGCG	GAA	CGCG	CGG	AAAG	CACT	CGT	CAT	CCAG	ATCT	1200
DB	1138	GCCTTT	CCGG	T	CGCG	GAA	CGCG	CGG	AAAG	CACT	CGT	CAT	CCAG	ATCT	1197
QY	1201	GAC	CTGT	CCAC	ACCG	CCCT	CG	AGCA	ATCT	CTCT	GT	TTTC	CGT	CGAC	1260
DB	1198	GAC	CTGT	CCAC	ACCG	CCCT	CG	AGCA	ATCT	CTCT	GT	TTTC	CGT	CGAC	1257
QY	1261	CCGAG	T	CCAC	CTC	AG	CGAT	CTC	CGCT	CCAG	GGG	CGT	CGCG	CCCG	1320
DB	1258	CCGGA	T	CCAC	CTC	AG	CGAT	CTC	CGCT	CCAG	GGG	CGT	CGCG	CCCG	1317
QY	1321	TTT	GAC	AGCG	AAATTC	CG	AGAT	TG	CTG	CGC	CTT	CAT	GAC	CTT	1380
DB	1318	TT	CGA	CAG	CGAAT	T	CG	AGAT	TG	CTG	CGC	CTT	CAT	GAC	1377
QY	1381	GAG	TT	CGT	G	A	CGG	TAC	AA	CAT	CA	CTT	CGA	CTG	1440
DB	1378	GAG	TT	CGT	G	A	CGG	TAC	AA	CAT	CA	CTT	CGA	CTG	1437
QY	1441	ACG	GAT	CTAC	AAG	T	CCG	CT	CGA	CGG	TAC	CGG	G	CGAT	1500
DB	1438	ACG	GAT	CTAC	AAG	T	CCG	CT	CGA	CGG	TAC	CGG	G	CGAT	1497
QY	1501	CGG	GT	TGG	G	ACAT	TCG	SC	CAG	AG	CA	CTT	T	CAGA	1560
DB	1498	CGG	GT	TGG	G	ACAT	TCG	SC	CAG	AG	CA	CTT	T	CAGA	1557
QY	1561	ATG	GT	G	AAC	AT	TG	A	CTG	ACG	G	AT	CA	CT	1620
DB	1558	ATG	GT	G	A										

QY 1621 CTGAACGCGCTGCGCGAGCGGCTCTTTGAAGCAAGAAGAGATCTGAGCTACCGGAC 1680
DB 1618 CTCACGCGCTGCGCGAAGCGTCTGAAGGACAAAGAGAGGACCTGAGCTATCGGAC 1677
QY 1681 ATCCCGCGCTACTAGCGCTTCGGGCGCGCGAGCGCGGGGTGATCGGGGAGTATTGTG 1740
DB 1678 ATCCCGCGCTACTAGCGCGCGCGGCGCGCGAAGCGGGGTGATCGGGGAGTACTGCATA 1737
QY 1741 CAGGACTCGCTGCTGGTGGGCGAGCTGTTCTTCAAGTTTCTGCGCGACCTCGAGCTTTC 1800
DB 1738 CAGGATTCCTGCTGGTGGGCGAGCTGTTTAAAGTTTTCCTCCATCTGAGACTCTG 1797
QY 1801 GCGGTGCGCGCTGCGGGGCAATCAACATCACCGCACCATCTACGACGCGCAGCATC 1860
DB 1798 GCGGTGCGCGCTTGGCGGGTATTAACATCACCGCGACCATCTACGACGCGCAGCATC 1857
QY 1861 GCGGTCTTACGTGCTCTCGGCTTCGGGCTTCGGGCGCAGAGGCTTCATCTGCGGACAC 1920
DB 1858 GCGGTCTTACGTGCTCTCGGCTTCGGGCGCAGAGGCTTCATCTGCGGCGACAC 1917
QY 1921 CAGGGGCGGTTTCGGGGCTTCGACAAAGAGGCGGCCAAGCGCCCGCGCGTGCCTCGGG 1980
DB 1918 CAGGGGCGATTAGGGGCGCGGGGGGAGGCGGCCAAGCGTTCGGGCGCAGCGCGGAG 1977
QY 1981 GAAGGGAGCGCGCGGGGACCGGAAACGGGACGAGGATAGAGACGACGAGGACGAG 2040
DB 1978 GACGAGGAGCGCGCAGAGGAGGAGGGGAGGAGC-----AGGACGAACGCGAGGAGGC 2031
QY 2041 GACGGGACGAGCGGAGGAGGTTCGCGCGAGACCGGGGCGCGGACGTTGGGTACGAG 2100
DB 2032 GGGGCGGAGCGGAGCGCGGCGCGGCGCGGAGACCGCGCGCGGACGCTGGGGTACCG 2091
QY 2101 GGGGCGCGGGTCTCGACCCCACTTCGCGGTTTACGCTGCGACCCGCTGGTGTGTTGAC 2160
DB 2092 GGGGCGAGGGTCTTGAACCCCACTTCGCGGTTTACGCTGAACCCCGGTTGTTGAC 2151
QY 2161 TTTGCCAGCTGTATCCCGAGCATCATCCAGGCCCAACACTGTGCTTTCAGTACGCTCTCC 2220
DB 2152 TTTGCCAGCTGTATCCCGAGCATCATCCAGGCCCAACACTGTGCTTTCAGTACGCTCTCC 2211
QY 2221 CTGCGGCGGAGCGGCTGCGCACCTTGAGGCGGACCGGAGCTACCTTGAGATCGAGGTG 2280
DB 2212 CTGAGGGCGGACGAGTGGCGCACCTTGAGGCGGCGCAAGGACTACCTTGAGATCGAGGTG 2271
QY 2281 GGGGCGCGACGCGCTGTTCTTCTGTAAGGCCCAACGCTAGCGAGAGCTGCTGAGCATCTG 2340
DB 2272 GGGGCGCGACGCGCTGTTCTTCTGTAAGGCTCAGGCTCAGCTGCGAGAGAGCTCCTCAGCATCTC 2331
QY 2341 CTGCGCGATGGCTGGCCATGCGAAGCAGATCCGCTGCGGGATCCCGGAGACACCC 2400
DB 2332 CTGCGGAGCTGGCTCGCATCGCAAGCAGATCCGCTCGCGGATTCGCCAGAGCAGCCCC 2391
QY 2401 GAGGAGCGGCTCTCTCGACAAAGCAAGCGCGGCATCAAGTGGTGTGCACTCGGGT 2460
DB 2392 GAGGAGCGGCTCTCTCGACAAAGCAGCAGCGCGGCATCAAGTGTGTTGTAATCTCGGGT 2451
QY 2461 TACGGGTTACCGGGGCGACACGCTTCTGCTGCTGCTGCTGACAGTGGCGCGCACCGCTG 2520
DB 2452 TACGGGTTACGGGAGCGACACGAGCTCTGCTGCTGCTGCTGACAGTGGCGCGACCGCTG 2511
QY 2521 ACACCATGCGCGCGAGATGCTCTCTCGACGCGCGGCTACGCTGACGCGCGCTGGGCG 2580
DB 2512 ACACCATGCGCGCGAGATGCTCTCTCGACGCGCGGAGTACGCTCAAGCGCGCTGGGCG 2571
QY 2581 GAGTTCATGCTGCTGGCGACTTTCGAGGCGGCGCGGATGCGCGCGCGCTGGGCG 2640
DB 2572 GCCTTCGAACAGCTCTTGGCGGATTTCCCGAGGCGCGGACATGCGCGCGCGCGGCC 2631
QY 2641 TACTCCATGCGCATCATCTACGGGAGACGAGCTCCATTTTCTGTTTGTGCGCGGCTC 2700
DB 2632 TATTCCATGCGCATCATCTACGGGAGACGAGCTCCATTTTGTGCTGTGCGCGGCTC 2691
QY 2701 ACGGCGCGGGCTGTTGGCCATGGGCGCAAGATGGCGGACCATCTCGCGCGCGCTG 2760

DB 2692 ACGGCGCGCGGCTGACGGCCATCGCGGACAAAGATGGCGGACCATCTCGCGCGCGCTG 2751
QY 2761 TTCCTCCCGCGATCAAGCTCGAGTCGAAAAAAGTTTCCAAAGAGTCTGCTCATCGCC 2820
DB 2752 TTTCTGCCCGCCATCAAACTCGAGTGGAAAAAGAGCTTCAACAGCTGCTGCTCATCGCC 2811
QY 2821 AAGAAAAAGTACATCGCGCTCATCTCGGGGGGCAAGATGCTCATCAAGGGGCTGATCTG 2880
DB 2812 AAGAAAAAGTACATCGGGCTCATCTAAGGGGTAAAGATGCTCATCAAGGGGCTGATCTG 2871
QY 2881 GTGCGCAAAAAAATACTGCGGTTTATCAACCGCACCTTCAGGGGCTTGGTCAAGCTGCTG 2940
DB 2872 GTGCGCAAAAAAATACTGCGGTTTATCAACCGCACCTTCAGGGGCTTGGTCAAGCTGCTG 2931
QY 2941 TTTTACGACGATACCGTATCCGAGCGCGCGCGGTTAGCGGAGCGCCCGCAGAGAG 3000
DB 2932 TTTTACGACGATACCGTATCCGAGCGCGCGCGGTTAGCGGAGCGCCCGCAGAGAG 2991
QY 3001 TGGCTGCGCGACCCCTGCGCGAGGAGTGCAGGCGTTTCGGGGCGCTCTCGTAGAGGCC 3060
DB 2992 TGGCTGCGCGACCCCTGCGCGAGGAGTGCAGGCGTTTCGGGGCGCTCTCGTAGAGGCC 3051
QY 3061 CATCGCGCATACCGACCCCGAGAGGAGCATCCAGGACTTTGTCTTCAACCGCGCAACTG 3120
DB 3052 CATCGCGCATACCGACCCCGAGAGGAGCATCCAGGACTTTGTCTTCAACCGCGCAACTG 3111
QY 3121 AGCAGACACCGCGCGGTACACCAAGGCGCTGCGGCCCTGACGCGGTATTTACAG 3180
DB 3112 AGCAGACACCGCGCGGTACACCAAGGCGCTGCGGCCCTGACGCGGTATTTACAG 3171
QY 3181 CTATGCGCGCGCGCGGAGTCCCGTTCATCAAGGACGAGTCCCGTACGTAGCTGCTG 3240
DB 3172 CTATGCGCGCGCGCGGAGTCCCGTTCATCAAGGACGAGTCCCGTACGTAGCTGCTG 3231
QY 3241 GCCCAGACCCCGAGGTAGAGGAGACGCTCGCGCGGTGCGCGCTTCCCGGAGCTAGAC 3300
DB 3232 GCCCAGACCCCGAGGTAGAGGAGACGCTCGCGCGGTGCGCGCTTCCCGGAGCTAGAC 3291
QY 3301 GCCCGCGCGCGAGGAGCGCGCGCGCGCGCGCGCGCTTCCCGGCGCGCGCGCGCGCG 3360
DB 3292 GCCCGCGCGCGAGGAGCGCGCGCGCGCGCGCGCGCTTCCCGGCGCGCGCGCGCGCG 3351
QY 3361 CCCCGGAGACGCGCTCGCATGCGACCCCGCGGAGCGGCTCCAAAGCCCGCAAGCTG 3420
DB 3352 CCCCGGAGACGCGCTCGCATGCGACCCCGCGGAGCGGCTCCAAAGCCCGCAAGCTG 3411
QY 3421 CTGCTGTCCGAGTGGCGGAGATCCCGGATACGCCATCGCCCGGGGCGTTTCGCTCAAC 3480
DB 3412 CTGCTGTCCGAGTGGCGGAGATCCCGATACGCCATTCGCCATTCGCCCTCGCCCTGAAC 3471
QY 3481 ACAGCATTTACTTCTCGACCTGCTGGGGGCGCGCTGCGTACGTTTCAAGGCGCTGTTT 3540
DB 3472 ACAGCATTTACTTCTCCACCTGTTGGGGGCGCGCTGCGTACATTTCAAGGCGCTGTTT 3531
QY 3541 GGAATAACCCCAAGATCACCGAGAGTCTGTTAAAGAGTTTATTCGCCAGACGTGGCAC 3600
DB 3532 GGAATAACCCCAAGATCACCGAGAGTCTGTTAAAGAGTTTATTCGCCAGTGTGGCAC 3591
QY 3601 CCCCGGAGACGCTGCGCGCGCTCAGGGCGCGCGGGTTCGGGCGCGGGGCGCGCGCG 3660
DB 3592 CCCCGGAGACGCTGCGCGCGCGCTCAGGGCGCGCGGGTTCGGGCGCGGGTGGGTCGCGCG 3651
QY 3661 GCTACGCGGAGGAACTCTGCAATGTTGATAGAGCTTTGATCTACTAGCATGA 3717
DB 3652 GCTACGCGGAGGAACTCTGCAATGTTGATAGAGCTTTGATCTACTAGCATGA 3708

RESULT 7
AAD30080
ID AAD30080 standard; DNA; 3708 BP.
XX
AC AAD30080;

XX DT 17-MAY-2002 (first entry)
 XX DE Herpes simplex virus (HSV1-F-M1) mutant DNA polymerase gene.
 XX KW Herpes virus; medicinal; therapy; binding domain; DNA polymerase gene;
 KW antiviral; enzyme; mutant; ds.
 XX OS Herpes simplex virus.
 XX FH Key Location/Qualifiers
 FT CDS 1..3708
 FT /*tag= a
 FT /product= "Mutant DNA polymerase"
 XX W0200206513-A2.
 XX PN 24-JAN-2002.
 XX XX 13-JUL-2001; 2001WO-US016525.
 XX PF 13-JUL-2000; 2000US-0218118P.
 XX PR 13-APR-2001; 2001US-0283880P.
 XX XX (PHAA) PHARMACIA & UPJOHN CO.
 XX PA Homa PL, Wathen MW, Hopkins TA, Thomsen DR;
 PI WPI; 2002-179800/23.
 XX DR P-PSDE; AAE18856.
 XX PT Selecting compounds that inhibit herpes viruses by comparing inhibitory
 PT concentration of a compound of interest that inhibits wild-type herpes
 PT virus and domain mutant herpes virus, and selecting compound of interest.
 XX PS Claim 25; Fig 5; 126pp; English.
 XX CC The present invention relates to a method for selecting compounds that
 CC inhibit herpes viruses. The method involves measuring IC 5.0 of compound
 CC of interest that inhibits wild-type herpes virus and domain mutant herpes
 CC virus mutant herpes virus which is the same strain as wild-type herpes
 CC with IC 5.0 of the compound inhibiting wild-type herpes virus
 CC the compound, where IC 5.0 of the compound of interest that inhibits
 CC mutant herpes virus is at least 3 times greater than IC 5.0 of the
 CC compound that inhibits wild-type herpes virus. The method is useful for
 CC selecting compounds that inhibit herpes viruses. The compound is useful
 CC for manufacture of medicinals for selectively treating diseases caused by
 CC herpes viruses such as herpes viral infection, or for selectively
 CC inhibiting herpes viruses, in a human host by administering a compound to
 CC human in need of such treatment, where the compound inhibits herpes
 CC viruses by interaction with the binding domain in the viral DNA
 CC polymerase, and IC 5.0 of the compound that inhibits a binding domain
 CC mutant herpes virus is at least 3 times, preferably 5 times greater than
 CC IC 5.0 of the compound that inhibits the wild-type herpes virus which is
 CC the same strain as the mutant herpes virus. The present sequence is
 CC Herpes simplex virus (HSV1-F-M1) mutant DNA polymerase gene
 XX SQ Sequence 3708 BP; 659 A; 1237 G; 1201 G; 611 T; 0 U; 0 Other;
 Query Match 82.1%; Score 3053.4; DB 6; Length 3708;
 Best Local Similarity 89.2%; Pred. No. 0;
 Matches 3317; Conservative 0; Mismatches 391; Indels 9; Gaps 2;
 Qy 1 ATGTTTTCGCGGGGGGGCCGACCTCCCGGGGGGAGTCCGGGGCTCGGGCGCG 60
 Db 1 ATGTTTTCGCGGGGGGGCCGCTGTCCCGGGGAGAAAGTCCGGGGCGAGGGCGG 60
 Qy 61 TCTGGGTTTTTGGCCCCCAACCCCGGGGAGCCACCCAGAGCGCACCGCCGCTTGC 120
 Db 61 TCCGGGTTTTTGGCCCCCGGGGCTGTGGGAGCGCGGCC---GGGAGCCCCGCTTGC 117
 Qy 121 CGCGCGGAGAACTTCTTAAACCCCCCACTCTCGCTCAGACCGGAGCGCAGCCAAAGGCCCCC 180

Db 118 TTGAGGCAAAACTTTTACAAACCCCTACCTCGCCCGAGTCGGGACGCAACAGAGCCGACC 177
 Qy 181 GGGCGGGCTCAGCGCCATAGCTACTACGAGTGCAGGAAATTTGATTTATCGCCCGC 240
 Db 178 GGGCCCAACAGCGCCATAGCTACTATAGGAATGCGATGAATTTGATTTATCGCCCGC 237
 Qy 241 CGTTTCGTGAGAGGACGCCCCCGGAGCAGCGCACCGGGGTCCACGACGCGCGCTC 300
 Db 238 CGGGTCTGGAAGAGATGCCCGCCGAGAGCGCGCCGGGTGCAAGCGTCACTC 297
 Qy 301 CGGCGCGCCCTAAAGTGTACTGCGGGGGGAGCAGAGCGGACCTCTCTCCGCTGGGGCCG 360
 Db 298 AAGCGCGCCCGCAAGGTGTACTGCGGGGGGAGCAGAGCGGACGCTCTCTCGCGTGGGTG 357
 Qy 361 GAGGGCTTCTGGCGCGGTGCTGCGCCTGTGGGGGGGTGCGGACCATGCCCCCAAGGGG 420
 Db 358 GCGGGTCTTGGCGCGGGCGCTCGCGCTGTGGGGGGCGGTGGACCAAGCCCGCGGGG 417
 Qy 421 TTGAGCCCCACCGCTCACCGCTTTTCCAGCTGTACGACATCTCTGGAGCAGCTGGGAACAGCG 480
 Db 418 TTCAAACCCACCGCTCACCGCTTTTCCAGCTGTACGACATCTCTGGAGAACGTGGAGCAGCG 477
 Qy 481 TACAGCATGCGCGCCCGCCAGCTTCCAGAGCGATTTTATGACCGCATCAGCGCGCGCGG 540
 Db 478 TACGGCATGCGCGCGCCCGCAGTTTCCAGCGCGGTTTATGAGCGCCATCACACGACGCGG 537
 Qy 541 ACGTCACTACCGCTTCTGGGTCTGAGCCCCGAGAGGCATCGCTGCGCGTTACGCTCTAC 600
 Db 538 ACGTCACTACCGCTTCTGGGCTGACTTCCGGAAGGCCACCGGGTGGCGGTTTACGTTTAC 597
 Qy 601 GGCACGCGGAGTACTTTTACATGAACAGCGGAGGTGGATCGGACCTTGCAGTGCCTG 660
 Db 598 GGCACGCGGAGTACTTTTACATGAACAGAGGAGGTGCGACAGGACCTTACAATGCGCG 657
 Qy 661 GCCCGCGCGATCTCTCGAGCGCTTGGCGGGCGCTTGGCGAGTCCGCGGGGGCGTGC 720
 Db 658 GCCCGCAGAGTCTCTCGAGCGCATGGCGCGCGCTTGGCGAGTCCCGGGCGCGTGC 717
 Qy 721 TTCGGGGCATCTCCGCGGACCACTTTCGAGCGGAGGTGCTGGAGCGCGCGCTGTAC 780
 Db 718 TTCGGGGCATTTCCGGGAGCACTTTCGAGCGGAGGTGCTGGAGCGCACCGAGCTGTAC 777
 Qy 781 TATTACGAAACGCGCGCGACCTTGTACTACCGGTCTTCTGTGCGAAAGCGGGCGCGGTG 840
 Db 778 TACTAGAGAGCGCGCGCTCTGTCTTACCGGTCTTACGCTCCGAAAGCGGGCGCGTGTG 837
 Qy 841 GCCTACTGTGCGACAACTTTTCCCGCGCATCAGGAAGTACGAGGGGGCGCTCGAGCGC 900
 Db 838 TCGTACTGTGCGACAACTTCTCCCGGCGCATCAAGAAAGTACGAGGGGTGGGTGCGAGCGC 897
 Qy 901 ACCACCGGTTTATCTTGGACAAACCCGGGGTGTGTACCTTTCGCTCGGTACCGCTCAAG 960
 Db 898 ACCACCGGTTTATCTTGGACAAACCCGGGGTGTGTACCTTTCGCTCGGTACCGCTCAAG 957
 Qy 961 CCGCGCGCGGGAAACGCGCGCGCCCAACCGCGCGCCCGCGAGCGGTTTCGGAACCTCGAGC 1020
 Db 958 CCGCGCGGAAACAAACAGCTAGCCCGCGCGCGCTTGGGCTTTCGGGACATCCAGC 1017
 Qy 1021 GAGTCCAGTTTAACTGACGCGGGAACAACCTGCGCTCGAGGGGGCGATGTGTGACTG 1080
 Db 1018 GAGTCCAGTTTAACTGATCGGCGGAAACAACCTGGCCATCGAGGGGGCGATGAGGACCTA 1077
 Qy 1081 CCGGCTTACAGCTCATGTGCTTCGATATCGAATGCAAGCGCGGGGGGAGGACGAGCTG 1140
 Db 1078 CCGGCTATCAAGCTCATGTGCTTCGATATCGAATGCAAGCGCGGGGGGAGGACGAGCTG 1137
 Qy 1141 GCCTTTCCGCTGCGGAAACCGCGCGGAAAGACCTCTGTATTCAGATCTCTGTCTCTCTAC 1200
 Db 1138 GCCTTTCCGCTGCGGGGCAACCGCGGAGACCTCTGTATTCAGATATCTGTCTCTCTAC 1197
 Qy 1201 GACTGTGCAACCAACCGCGCTCGAGACATCTCTCTGTGTTTTCGCTCGGATCTCTCGACCTC 1260

Db 2992 TGGCTGGCGGACCCCTGCCGAGGACTGACGGCTTCGGGGCGCTCTCGTAGACGC 3051
 Qy 3061 CATCGCGCATCACCGACCCGAGAGGAGATCCAGGACTTTGCTCTCAGCGGCACTG 3120
 Db 3052 CATCGCGCATCACCGACCCGAGAGGAGATCCAGGACTTTGCTCTCAGCGGCACTG 3111
 Qy 3121 AGCAGACACCGCGCGGTACACCAACAAGCGCTGCGCCACTGACGGTGTATTACAAG 3180
 Db 3112 AGCAGACACCGCGCGGTACACCAACAAGCGCTGCGCCACTGACGGTGTATTACAAG 3171
 Qy 3181 CTCATGCCCCCGCGCGCGAGTCCCTCCATCAAGGACCGGATCCCGTACGTGATCGT 3240
 Db 3172 CTCATGCCCCCGCGCGCGAGTCCCTCCATCAAGGACCGGATCCCGTACGTGATCGT 3231
 Qy 3241 GCCAGACCCGCGAGGTAGAGGAGCGGTGCGCGGTGCGCGCTCCCGGAGCTAGAC 3300
 Db 3232 GCCAGACCCGCGAGGTAGAGGAGCGGTGCGCGGTGCGCGCTCCCGGAGCTAGAC 3291
 Qy 3301 GCGCGCCCGCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3360
 Db 3292 GCGCGCGCGCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3351
 Qy 3361 CCCCGGAGACCGCTCGCATGCGACCCCGCGGAGCGCGCTCCAAAGCCCGCAAGCTG 3420
 Db 3352 CCCCGGAGACCGCTCGCATGCGACCCCGCGGAGCGCGCTCCAAAGCCCGCAAGCTG 3411
 Qy 3421 CTGGTGTCCGAGCTGGCGGAGGATCCCGGCTACGCCATCGCGGGCGTTCGCTCAAC 3480
 Db 3412 CTGGTGTCCGAGCTGGCGGAGGATCCCGGCTACGCCATCGCGGGCGTTCGCTCAAC 3471
 Qy 3481 ACGGACTATTACTTCTCGCACTGCTCGGGCGCGCTCGCTGACGTTTCAAGGCGCTGTT 3540
 Db 3472 ACGGACTATTACTTCTCGCACTGCTCGGGCGCGCTCGCTGACGTTTCAAGGCGCTGTT 3531
 Qy 3541 GGAATAACCGCAAGATCACCGAGTCTGTATAAGAGTTTATTCGCGAGACGTGGCAC 3600
 Db 3532 GGAATAACCGCAAGATCACCGAGTCTGTATAAGAGTTTATTCGCGAGTGTGGCAC 3591
 Qy 3601 CCCCGGAGACCGTGGCGCGCGCTCAGGGCGCGGGTTTCGGCGCGCGGGCGCGCGCG 3660
 Db 3592 CCCCGGAGACCGTGGCGCGCGCTCAGGGCGCGGGTTTCGGCGCGCGGGCGCGCGCG 3651
 Qy 3661 GCTACGCGGAGGAACTCTGTCGAATGTTGATAGAGCTTTGATCTCTAGCATGA 3717
 Db 3652 GCTACGCGGAGGAACTCTGTCGAATGTTGATAGAGCTTTGATCTCTAGCATGA 3708

RESULT 9
 ID ADP74211/c
 XX ADP74211 standard; DNA; 149158 BP.
 AC ADP74211;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Equine herpesvirus 1 genome gM deletion mutant #2.
 XX
 DE virucide; vaccine; Equine Herpes Virus; EHV; gM; vaccine;
 KW EHV-associated condition; Equine herpesvirus 1; EHV1; ds; mutant; mutein.
 KW
 OS Equine herpesvirus 1.
 XX
 OS Synthetic.
 XX
 PN US2004109873-A1.
 XX
 PD 10-JUN-2004.
 XX
 XX 21-JUL-2003; 2003US-00624149.
 PF
 XX 19-JUL-2002; 2002DE-01033064.
 PR
 PR 14-AUG-2002; 2002US-0403282P.
 PR
 PR 11-APR-2003; 2003DE-01017008.
 XX

PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
 XX Neubauer A, Ziegler C;
 PI WPI; 2004-440311/41.
 XX
 PT New recombinant equine herpes (EHV) virus free of heterologous elements,
 PT and where protein gM has been deleted, useful as a vaccine for treating
 PT or preventing EHV infections.
 XX
 PS Claim 9; Page; 156pp; English.
 XX
 CC The invention describes a new recombinant Equine Herpes Virus (EHV) where
 CC the protein gM is absent, and the EHV is free of heterologous elements.
 CC Also described are: a nucleic acid coding for an EHV defined above; a
 CC vaccine preparation comprising the EHV or nucleic acid; obtaining a
 CC recombinant EHV; and a cell line for use in the method, where the gene
 CC encoding the protein gM is transfected into the cell line, and the cell
 CC line expresses gM. The vaccine comprising the EHV or nucleic acid
 CC encoding EHV is useful for treating and/or preventing EHV-associated
 CC condition, and for monitoring the therapeutic success. The recombinant
 CC EHV is useful as a vaccine against EHV infections. This sequence
 CC represents an Equine herpesvirus 1 genome in which nucleotides 93268-
 CC 94322, comprising regions of the gM gene, have been deleted.
 XX
 SQ Sequence 149158 BP; 32350 A; 42892 C; 41659 G; 32257 T; 0 U; 0 Other;
 Query Match 29.7%; Score 1104.8; DB 12; Length 149158;
 Best Local Similarity 59.1%; Pred. No. 1.6e-169;
 Matches 2131; Conservative 0; Mismatches 1317; Indels 156; Gaps 8;
 Qy 186 GGCCTCAGCGCATACGTACTACAGCGAGTGCAGCAATTTATCGATTTATCGCCCGCTTC 245
 Db 55065 GCCCCCCCAACATCTGCTACTGACAGGTTGGTAGCTTTAAGTTTATAGTCCAAATG 55006
 Qy 246 GCTGGAAGAGGACGCGCGCGGAGCAGCGACCGGGGTCACAGCGCGCTTCGCGCG 305
 Db 55005 CCTCGATGAAGAAGCGCGCGCGGACGACGCGGTGTACAGCTGGCGCACCTTGGAGCG 54946
 Qy 306 CGCCCTTAGGTACTGCGGGGGGACGAGCGGAGCTCTCGCGTGGCGCGCGGAGG 365
 Db 54945 CCCACCCAAAGTACTGCGATGGCTCAGAGTACGAGCTGTAACCTTTCCTCCGAGG 54886
 Qy 366 CTTCGCGCGCTCGCTTGGCGCTGTGGGCGGTGGGACCATCGCCCGCCAAAGGGTTCTGA 425
 Db 54885 TTGCTGGCTCGCAGGATTCGGGTGTGAACGCCAGGATTTTCGGGGCGATGGAATCAA 54826
 Qy 426 CCCCAACCGTCACCGTCTTCCACGTGTACGATCTCTGGAGCAGCTGGAAACACGCGTACAG 485
 Db 54825 CCCAGATTTGAGAGATTTTCACTGTACGACATAGTAGAGACTTCGGAGAGCGCTCACA 54766
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 Db 54765 CGATGACCCATCCAGGTTTCTGAGCTAT-----CCGCGCCAAAGCGGTCTGT 54718
 Qy 546 CATCAGCTTCTGGGTCTGACCCCGGAGGCGCATCGGTCGCGCTCCGCTTACGTCACGCGAC 605
 Db 54717 GGTAACTACTCTGGGATGAGCGAGTGTGAAGCGAGTCTCGCTTACGCTATGCTGT 54658
 Qy 606 GCGCGAGTACTTTTACATGAACAAAGCGGAGGTGGATCG-----644
 Db 54657 GCGCCATTTATTTTACATGGCAAAGCGGAGGTGGATAGCGCTTGTGGAATAAACCCGA 54598
 Qy 645 -----GCACCTGAGTGGCGTCCCGCGCG-----GATCTCT 676
 Db 54597 GGCAGAACTCTGCGCGCAATGTTGAGTCTCGCGCAAGCTCGGCTTTGAGCGCGGCTCT 54538
 Qy 677 GCGAGCGCTTGGCGCGCGCGCTCGCGAGTCTCGCGGGGGCGCTGTTCCGCGG-----728
 Db 54537 GGGAAATGGCAACGGCGGCAACAGAGCGCGCGGAGTGTGGGGCGGAAA 54478
 Qy 729 ---CATCTCGCGGACCACTTCGAGCGGAGGTGGTGGAGCGCGCGCTGTACTATTATTA 785

Db 54477 GCACGTGTCTGGGACTGCTTCAAGTAGTGAGACCGGTGTGTCACACGACGCTGTACTT 54418
Qy 786 CGAAACGCGCCCGACCCCTGTACTACCGGCTCTTCTGTGGAAGCGGCGCGCTGGCCTA 845
Db 54417 TGGATCTAAGCCAGCTCTCTACTATAGATATCTGCCTCCAGCAGCGCCTTGGAGGGTT 54358
Qy 846 CTTGTGCGACAACTTTTCCCGCGGATCAGGAAGTACGAGGGGGGCTGCGACGCAAC 905
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Db 54297 CGGCTGTGTGTGACATGAATTTTACGATTTCCGGTGTGTACCGCTTGCACCCGG 54238
Qy 966 CCGGGGAAACGCGCGGCCCAACCGCGCCCGCCGACGCGGTTTCGAAACCTCGACGACGT 1025
Db 54237 CACCCAGGAGCGTGTCAACTTCGCCCCGTTGAGCGACACGTCACCTCAAGCGAGCT 54178
Qy 1026 CGAGTTTAACTGACGGCGGACAACTTGGCCGCTCGAGGGGCCATGTGTGACCTGCGCGC 1085
Db 54177 GGAGATTAACTGTACTCCCGATAACCTGGAGCCGATACAGACGAGGCTGCTGGCCCGA 54118
Qy 1086 CTACAAGCTCATGTCTCGATATCGAATGCAAGCGCGGGGGGAGGACGAGCTGGCCTT 1145
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Qy 1146 TCCGGTCCGGAACCGCCGGAAGACCTCGTCATCCAGATCTCTGTCTGTCTACGACCT 1205
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Qy 1206 GTCCACCAACCGCTCGAGACATCTCTCTGTTTTTTCGCTGGATCTCGACACTCCCGA 1265
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Qy 1266 GTCCCACTCAGCGATCTCGCTCCAGGGCTCGCGGCCCTCGCTCTGCTGGATTGA 1325
Db 53937 GGAATCTCTGTTGATGCTCCAGCGCGGAGCCAGACCGGTTTGGAGTTGA 53878
Qy 1326 CAGGAAATTCAGATGTCTGGCTTCATGACCTTCGTCAAGCAGTACGCGCCCGAGTT 1385
Db 53877 CAGGAGTACGAGCTGTGTTGCTTCTTGACCTTCTCAAGCAGTACTCTCCGAGTT 53818
Qy 1386 GTGACCGGGTACAACTATCATCTTCACTGCGCTTCTGCTGACCAAGCTGACGGA 1445
Db 53817 CGCCACCGGGTACAACTATCTGTTAATTTGACTGGCGGTACATAGTTAAACAGGTAAAGTC 53758
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Db 53757 GGTGTATAACATCAAGCTGGACGGGTACGGCAAGTTCAACAAAGGGGGGCTGTTTAAGGT 53698
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Db 53697 GTGGACATCGCCACGAACCATTTTCAGAGAAGAGCAAGGTGAATCAATGSCCTGAT 53638
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Qy 1626 CGCGCTCGCGAGCGCTTGTGAAGBACAAGAGAAGATCTGAGCTACCGCGACATCCC 1685
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Qy 1686 CGCCTACTAGCCTCCGCGCCGCGCAGCGGGGTGATCGGCGAGTATTGTGTGACGGA 1745
Db 53517 CTCCTATTAACGGGAGGGCTGACCGAGGGGCTAATAGGAGATTGTATCCAGGA 53458
Qy 1746 CTCGCTCTGTGGGAGCTGTTCTTCAAGTTTCTCCGCACTGAGAGCTTTCCGCGT 1805
Db 53457 CTCCTAGGCTGTGGGCAAGCTGTTTTTAAAGTACCTCCCCCATCTGGAATCTATCGGCGGT 53398
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Db 53397 GGCCAAACTCGCCCGTATCAACCTTAACCGGGGTAAATTTTGAACGGTTCAGCAAAATTCGCT 53338

Qy 1866 CTTTCACTGCTCTCTGCGCTTGTGGCGCCAGAGGGCTTTCATCTGCGGACACCCAGG 1925
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Qy 1979 -----GGGAAGGGAGCGCGCGGGGACGGAAACGGGAGCAGGATAGGACGACGGA 2033
Db 53217 AAGCCACGCTTTCAGACATCAGACGAACCCGACGCTGTGACGCTACCCCGAGCGCGC 53158
Qy 2034 GGACGAGACGCGGACGAGCGCAGGAGGTTCGCGCGGAGACCGGGGGCCGCGACGTTGG 2093
Db 53157 AGGATCTGGCGCTACTTCTGAAACGGAGCGGGAAGCCCGCTGCGGAGGCGCTGG 53098
Qy 2094 GTACAGGGGGCCCGGCTCTCGACCCCACTCTCGGGTTTTTCACTGACACCCGTTGGT 2153
Db 53097 CTACAGGGAGCAAGGTTCTTAGACCCGCTATCCGGCTTTTCACTGGAACCCCGTTGGT 53038
Qy 2154 GTTTGACTTTGCGACGCTGTACCCAGCATCATCCAGGCCCAACCTGTGCTTTCAGTAC 2213
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Qy 2214 GCTCTCCTCGCGCCCGAGGCGCTGCGGCACCTTGAGCGGACCGGACTACTCTGGAGAT 2273
Db 52977 CTTGGCGCTCGATGAAGTGGATCTGGCGGGCTTCAACCATCTCGCTGACTACTCGAGCT 52918
Qy 2274 CGAGGTGGGGGGCGACGCTGTTTCTGTAAGGCCCAAGTACGCGAGAGCTGCTGAG 2333
Db 52917 CGAGGTGGGTGACCAAAAGTTATTTTGTGTCACGCCCATATTCGCAAAAGCTGCTGG 52858
Qy 2334 CATCTGCTCGCGACTGCTGGCCATGCGAAAGCGGTGAGGCGCGGAATCCCCACCAG 2393
Db 52857 CATCTGCTCGCGACTGCTGGCCATGCGAAAGCGGTGAGGCGCGGAATCCCCACCAG 52798
Qy 2394 CACCCCGAGGAGCGCTCTCTCGACAAAGCAACAGCGCGCCATCAAGGTGGTGTGCA 2453
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Db 52737 CTGCTTACGATTTACCGGGGGTGGCAACCGCTGTTGCGCTGCTGAGGATAGCGCG 52678
Qy 2514 CACGTTGACCACTCGCGCGCGAGATGCTCTCGACGCGCGCGCTGCTGCTGCTGCTGCTG 2573
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Db 52617 TTGGCGGACGCGCGAGCTGCTGGAGGACATTTTCCAGGGGCTATAGTTTCCGAACCA 52558
Qy 2634 CGGTGCGTACTCCTATGCGCATCATCTACGGGGACACGATCTCAATTTTGTGTTGCTGCG 2693
Db 52557 CAAGCTTACTCGCTCAGGGTATCTACGAGACACCGACTCTCGCTGTTTATCAAGTTGT 52498
Qy 2694 CGGCTCAGCGCGCGGCTTGGCCATGGGGCAAAAGTGGCGAGCCACATCTCGG 2753
Db 52497 GGGCTGACGTAAGGGGGGTATCGGAGCTGGGGGATGCTATGTCGCTCAGATTTCAGC 52438
Qy 2754 CGGCTGTTCTCTCCCGGATCAAGCTCGAGTTCGAAACAAAGTTTCAACAGCTGCTGCT 2813
Db 52437 GGACCTCTTTAGAGCGCCATCAACTGGAGTGTGAGAGACCTTTTCAGCGACTGCTGCT 52378
Qy 2814 CATCGCAAGAAAGTACATCGCGCTCATCTCGGGGGCAAGATGCTCATCAAGGGCGT 2873
Db 52377 GATCACCAAGAAAGTACATAGTGTGTATAAACGGGGGGAAGATGCTCATGAAGGGGT 52318
Qy 2874 GGATCTGGTGGCAAAACAACTCGCGGTTTATCAACCGCACCTTCCAGGGCCCTGCTGCA 2933
Db 52317 CGACCTGGTCCCAAAATAACTGCTCTTTCATTAACCTTGTACGCGCGCATCTGGTAGA 52258

Qy 2934' CTTGCTGTTTACGACGATACCGTATCCGAGCGCGCCGCTTGTACCGAGCGCCCGC 2993
 Db |||||
 52257 TCTTTTGTGTACGACGAGGATGTGGCCACGGCGGACGAGGTGACAGACGTGCTCC 52198
 Qy 2994 AGAGGAGTGTGCGCGGACCCCTGCGCCGAGGACATGACGGCTTGTGGGCGCGTCTCGT 3053
 Db |||||
 52197 CGCAGAAATGCGTGGGCGCGCTTACCGAGCGGCTTTGACAAGTTTGGGCGAGTGTGCTGT 52138
 Qy 3054 AGACGCCATCGCGGATACCGACCGGAGAGGACATCCAGGACTTTGCTCTCACCGC 3113
 Db |||||
 52137 AGAGCGGTACAACGCTATCACTGCCCCCACTTGGAGGTGGCGAGTTCCTTATGACTGC 52078
 Qy 3114 CGAACTGAGCAGACACCGCGCGGTACACCAACAGCGCTGCGCCACCTGACGGTGA 3173
 Db |||||
 52077 TGAGCTGAGCGCTCACCGAATCGTATACCAACAGCGCTGCGCCACCTCACCGTCTA 52018
 Qy 3174 TTACAGCTCATGCGCGCGCGGAGTCCCGTCCATCAAGACCGGATCCGCTACGT 3233
 Db |||||
 52017 CTTTAACTCGCCATGAGGAATGAAGAACTGCGCAGCGTAAAGAGAGAATTCGCTATGT 51958
 Qy 3234 GATCGTGGCCAGACCCCGAGGTAGAGAGACGGTCCGCGGCTGGCGCCCTCCGCGA 3293
 Db |||||
 51957 GATAGTTCGCGAGACC-----GAGGCCCGGAGACGCGA 51925
 Qy 3294 GCTAGACCGCGCGCGCGGACGAGCCCGCGCCCGCGGCGCTGCTCCCGCGC 3353
 Db |||||
 51924 AGCGGTGTAGTAACTCAATGCGCGGTACGCGCCAAACCCCGTGTGTAAACAGACCGC 51865
 Qy 3354 CAAGCGCCCGGAGAGACCGCTGCGATCGGACCCCGGAGGCGGCTCCAGACCCCGC 3413
 Db |||||
 51864 ACGCCCGCAACCTAA-----ACG 51847
 Qy 3414 CAGACTGCTGTGTCGAGTGGCGGAGGATCCGGGTACGCCATCGCCCGGCGGCTTCC 3473
 Db |||||
 51846 CAAACTGCTGTTCGACCTCGCGGAGACCGACCTATGTTCGAGAAATGACGTACC 51787
 Qy 3474 GCTCAACACGAGCTATTACTTCTCGACCTGCTGGGGCGCGCTGCGTGAAGTTCAGGC 3533
 Db |||||
 51786 GCTAAACACAGACTACTATTCTCCACCTGTTGGGTACCAATAGCGTGACCTTTAAGGC 51727
 Qy 3534 CTTGTTGGAAATACCCGAGATCACCGAGAGTCTGTTAAAGGTTTATTCGCGAGAC 3593
 Db |||||
 51726 TCTATTGCGAAATGATGAGAACACAGAAATCTTTTAAAGCGGTTTATTCGCGAAAC 51667
 Qy 3594 GTGSCAC--CCCGCGACGAGTGGCGCGGCTCAGGGCGCGGGGTTTCGGCGCGC 3650
 Db |||||
 51666 CCCCCAAGACCCCGAAGAACCCAGGCACTGCTTGAGCGCGCGGCTTTGAAAGCT 51607
 Qy 3651 GGGGCGCGGCTACCGCGGAGGAACTCGTGAATGTTGATAGACCTTTGATACTCT 3710
 Db |||||
 51606 GACGCCCTTTACACCGGAGGAGAAAGTCTGCGAATACTGCATACAGTTTTTTGCTACTCT 51547
 Qy 3711 AGCA 3714
 Db |||||
 51546 AGAA 51543

RESULT 10
 ADP74212/c

ID ADP74212 standard; DNA; 149261 BP.

XX

AC ADP74212;

XX

DT 26-AUG-2004 (first entry)

XX

DE Equine herpesvirus 1 genome gM deletion mutant #3.

XX virucide; vaccine; Equine Herpes Virus; EHV; gM; vaccine;

KW EHV-associated condition; Equine herpesvirus 1; EHV1; ds; mutant; mutuin.

XX

OS Equine herpesvirus 1.

OS Synthetic.

XX

PN US2004109873-A1.
 XX
 PD 10-JUN-2004.
 XX
 PF 21-JUL-2003; 2003US-00624149.
 XX
 PR 19-JUL-2002; 2002DE-01033064.
 XX
 PR 14-AUG-2002; 2002US-0403282P.
 PR
 PR 11-APR-2003; 2003DE-01017008.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
 XX
 PI Neubauer A, Ziegler C;
 XX
 XX WPI; 2004-440311/41.
 XX
 PT New recombinant equine herpes (EHV) virus free of heterologous elements,
 PT and where protein gM has been deleted, useful as a vaccine for treating
 PT or preventing EHV infections.
 XX
 PS Claim 10; Page; 156pp; English.
 XX
 CC The invention describes a new recombinant Equine Herpes Virus (EHV) where
 CC the protein gM is absent, and the EHV is free of heterologous elements.
 CC Also described are: a nucleic acid coding for an EHV defined above; a
 CC vaccine preparation comprising the EHV or nucleic acid; obtaining a
 CC recombinant EHV; and a cell line for use in the method, where the gene
 CC encoding the protein gM is transfected into the cell line, and the cell
 CC line expresses gM. The vaccine comprising the EHV or nucleic acid
 CC encoding EHV is useful for treating and/or preventing EHV-associated
 CC condition, and for monitoring the therapeutic success. The recombinant
 CC EHV is useful as a vaccine against EHV infections. This sequence
 CC represents an Equine herpesvirus 1 genome in which nucleotides94263-
 CC 93302, comprising regions of the gM gene, have been deleted.
 XX
 SQ Sequence 149261 BP; 32381 A; 42917 C; 41687 G; 32276 T; 0 U; 0 Other;

Query Match 29.7%; Score 1104.8; DB 12; Length 149261;
 Best Local Similarity 59.1%; Pred. No. 1.6e-169;
 Matches 2131; Conservative 0; Mismatches 1317; Indels 156; Gaps 8;
 Qy 186 GGTCTAGCGCCATACGTACTACAGGAGTCCGAGGAATTTTCGATTTATCCCGCGTTC 245
 Db 55065 GCCCCCCCAACACTCGTACTGTCACAGAGTGGGTAGCTTTAAGTTTATAGCTCCAAGATG 55006
 Qy 246 GCTTGGAGAGGAGCGCCCGCGGAGCAGCGACCGGGGTCCAGACCGCGCGCTCCCGCGC 305
 Db 55005 CCTCATGAAGAAGCCCCCGCCGACGACGCGGTGTACACGTGGGACCTTGGAGCG 54946
 Qy 306 CGCCCCCTAAGGTGTACTGCGGGGGGACGAGCGCGAGCTCCTCCGCGTGGGCGCGGAGGG 365
 Db 54945 CCCACCCAAAGTGTACTGCGATGGCTCAGAGTACGACGTCTGAACCTTTGCCCTCCGAGG 54886
 Qy 366 CTTCTGGCGCGCTGCTTGGCGCTGTGGGCGGTGGGACCATGCCCGCCCAAGGGGTTCGA 425
 Db 54885 TTGCTGGCGCTCGCAGGATTCGGGTTTGGAACGCCACGAGGATTTTCGGGGCGATGGAATCAA 54826
 Qy 426 CCCACCGCTCACCGTCTTCCACGTGTACGACATCTCTGGAGCAGCTGTGAAACACCGGTACAG 485
 Db 54825 CCCAGATTTGAGAGATTTACGCTGTACGACATAGTAGAGACTTCGAGAGCGGCTCACA 54766
 Qy 486 CATGCGCGCGCCCGAGCTCCACGAGCGAATTTATGGACGCCATACGCCCGCGCGGACCGT 545
 Db 54765 CGATGACCCATCCAGGTTTGTCTGAGCTAT-----CCGCGCAAGCGGCTCTGT 54718
 Qy 546 CATCAGCTTCTGGTCTGACCCCGGAGGCCATCGCGTCCGCTTCACGCTACGCGAC 605
 Db 54717 GGTAACACTCTCGGGAATGAGCGAGTGTGAAAGCGAGTCCGGTTTCCGCTCTATGTTGT 54658
 Qy 606 GCGGCACTACTTTTACATGAACAGGCGGAGGTGGATCG----- 644
 Db 54657 GCGCCATTATTTTACATGTCMAAGCGGAGGTGATAGCGCTTGTGGAATAACACCGA 54598

QY	645	-----GCACCTGCAAGTGCCTGCCCCGCGC-----GATCTCT	676	Db	53517	CTCCTATTACCGGAGGGCTGACCGGAGGGCGTAAATGAGAGAGTATTGTATCCAGGA	53458
Db	54597	GGCAGAACTGTGCGCGCAATGGTGAATGCGCGCACAGCTCGGCTTTGAGCGCGCCCT	54538	QY	1746	CTCGTCTGCTGGTGGGAGCTGTTCTTCAAGTTCGCGCACCTGGAGCTTTCGCGCGT	1805
QY	677	GGGAGCGCTGGCGGGGCGCTGCGGAGTGCCTGGGGGCGTGTTCGCGG-----728	728	Db	53457	CTTAGGCTGGTGGGCAAGCTGTTTTTAAAGTACTCTCCCATCTGGAACTATCGCGCGT	53398
Db	54537	GGGAAATGGCAACGGCGGCAACAGAGCGGCGGACGCGCGGGGATGGTGGGCGGAAA	54478	QY	1806	CGCGCGCTGGCGGCGATCAACATCACCGCACCATCTACAGCGGCGAGCAGATCCGCGT	1865
QY	729	---CATCTCCGCGGACCACTTCGAGCGGAGGTGGTGGAGCGCGCGCGATGTACTATTA	785	Db	53397	GGCCAAACTCGCCGATATCACCTTAAACGCGGGTAAATTTTTCGCGTGAAGAAATTCGGT	53338
Db	54477	GCACGTGTCTGGGACTGCTTCAAGTGGAGACCGTGTGCCACAGACGCTGTACTATT	54418	QY	1866	CTTCACTGCTCTCTGCGCTTTCGCGGCGAGAAAGGGCTTCTATCTGCGCGACACCAAGG	1925
QY	786	CGAAACGCGCGGACCTCTGTACTACCGCTCTTCGTGCGAAGCGGCGCGCTGCGCTA	845	Db	53337	GTACACGCTGCTGTGTAATCTCGCCGCGAGAGAAAATTTTATTTTTCGCGACAAACAGACG	53278
Db	54417	TGGATCTAAGCGAGCTCTCTACTATAGAGTATCTGCCTCCAGACGCGCTGGAGGGT	54358	QY	1926	GCGGTTTTCGGCGCTTCGACAGAGGAGCGCCAAAGCGCGCGCGCTGCTCGG-----1978	1978
QY	846	CCTGTGCGACAACTTTTCCCGCGATCAGGAGTACGAGGGGGGCTCGAGCGCACAC	905	Db	53277	CCGGTTTGAACAGTCAGGAGACGCGCGTCAAGACTTTTCGAGTTTGGCTATGGATAGCCA	53218
Db	54357	CATCTGCGACAACTTTTCAACCGGAGATTAACAAATTCAGAGGGAGCGTGGACGAC	54298	QY	1979	-----GGGAGGGGAGCGCGCGGCGAGCGGAAACGGGAGCGAGGATAAGGACGACGAGA	2033
QY	906	CCGGTTTATCTTGGAACAAACCGGGGTTTGTCACTTTCGGCTGGTACCGCTCAAGCCCGG	965	Db	53217	AAGCCACGCTTTCGACAGTACAGACGAAACCGACGCGTGTGACGCTACCCCGGACGCGC	53158
Db	54297	GCGCTGTGTTGGACATGAATTTTACAGTTTTCGGTGGTACCGCTTCGACCGCG	54238	QY	2034	GGAAGAGAACGGGAGACGAGCGGAGGTCGCGCGCGAGACCGGGGCGCGGCACTGTGG	2093
QY	966	CGCGGGAAACGCGCGCGCCCAACCGCGCCCCCGGACGCGGTTTCGAACTTCGAGCGAGT	1025	Db	53157	AGGATCTGGCGCTACTTCTGAAACCGGAGCGGGAAGCCCGCGTTCGAGGGCGCGTGG	53098
Db	54237	CACCCACGAGAGCGTGTCAACTTCGCGCGGTTGAGCGACACGCTCACCTCAAGCGAGT	54178	QY	2094	GTACAGGGGCGCGGCTCTCGACCCACCTCCGGGTTTCACTGCGACCGCGTGGTGGT	2153
QY	1026	CGAGTTTAACTGACGCGGACCACTTCGCGCTCGAGGGGGCCATGTGTGACCTGCGCGC	1085	Db	53097	CTACAGGGAGCAAGGTTCTAGACCCCGCTATCCGGCTTTTTCATGTGGACCCCGTGGTGT	53038
Db	54177	GGAGTTAACTGTACTCCCGATACCTGGAGCGCGATACGACGAGGCTGCTCGGCCGA	54118	QY	2154	GTTTGACTTTTCCGACCTGTACCCAGCATCATCCAGGCCCAACCTGTGCTTCAGTAC	2213
QY	1086	CTCAAGCTCATGTGCTTCGATATCGAATGCAAGCGCGGGGAGGACGAGCTGGCTT	1145	Db	53037	GTTTGACTTTCGCTAGCTTATACCCAGCATTTATCCAGGCCCATTAACCTCTGTTTACCAC	52978
Db	54117	CTATAAGCTCATGTGCTTTGATATAGAGTGTAAAGCTGGAACGGGTAAAGAAATGGCGT	54058	QY	2214	GCTCTCCTGCGGCGCGAGCCGTCGCGCACCTGGAGCGGACCGGGACTACTCTGGAGAT	2273
QY	1146	TCCGGTCCGGAAACGCCCGGAAGACCTCGTATCAGATCTCTGTCTGTCTACGACCT	1205	Db	52977	CCTGGCGCTCGATGAAGTGGATCTGGCGCGGCTTCAACCATCCGTCGACTACTCGACGTT	52918
Db	54057	CCAGTGGCAACTAACCAAGAGGACCTGGTCAATCCAGATCTCCTGTCTGTACTGCT	53998	QY	2274	CGAGTGGGGGCGGACGCGCTGTTCTGTGAAGGCCCATGTCGCGAGAGCGCTGTAG	2333
QY	1206	GTCCACACCGCTCGAGGACATCTCTGTTTTCGCTCGGATCTCGGACCTCCCGGA	1265	Db	52917	CGAGTGGGTGACCAAAAGTTATTTTGTCCACGCCCATATTCGCGAAAGCGCTGCTGG	52858
Db	53997	TGCTACTCAGAACCAAGGACACCTGCTGTTTTCCTCGGGTCATGCGATATCTCTGA	53938	QY	2334	CATCTCTGCTGCGGACTGGCTGGCATGCGAAAGCAGATCCGCTCGCGGATCCCGCAGAG	2393
QY	1266	GTCCACCTCAGCGATCTCGCTCCAGGGGCTCGCGGCGCTCGCTGCTGGAAGTTGA	1325	Db	52857	CATCTTCTGCTGCGGACTGGCTGGCCATGCGGAAAGCGGTGAGGGGCGAAATCCCGACAG	52798
Db	53937	GGATACTCTGTTGATCGCTCCAGCGGCGGAGCCGAGCGGTTTGGAGTTGA	53878	QY	2394	CACCCCGAGAGGCGCTCTCTCGACAAAGCAACAGCCGCCATCAAGGTGGTGTGCAA	2453
QY	1326	CAGCGAATTCAGATGCTGTGGCTTCATGACCTTCGTCAAGCAGTACGCGCCCGAGTT	1385	Db	52797	CACCCCGAGAGGACGTTTACTAGATTAAGCAGCAGTCTCGATTAAGGTGATATGCAA	52738
Db	53877	CAGCGAGTACGAGCTGCTGTGCTTCTGACCTTTCTCAAGCAGTACTCTCCCGAGTT	53818	QY	2454	CTCGGTGTCAGGGTTTACCGGGGCGAGCAGGCTTCTGCGCTGCTGCGCTGCGAGCGCGC	2513
QY	1386	CGTACCGGGTACACATCATCACTTCACTGCGCCCTTCTCTGCTGACCAAGCTGACGGA	1445	Db	52737	CTCGGTGTCAGGATTCAGGGGTGGCAACGGGCTGTTCGCTGCTGAGGATAGCGCGC	52678
Db	53817	CGCCACCGGCTACAACTCATGTTTGAATGCTGGGCGTACATGTTAAACAGGTAAAGTC	53758	QY	2514	CACCGTGAACCACTCGGCGCGGAGATGCTCCTCGGACGCGCGCTGCTGCGAGCGCGC	2573
QY	1446	GATCTCAAGGTCCCGCTCGACGGGTACGGCGGATGAACGGCGGGGTGTTCGCGGT	1505	Db	52677	TACCGTTACCAAGATAGGACGCGACATGCTCCTCAAGACCCGAGATTAAGTTCACTCTCG	52618
Db	53757	GGTGTATTAACATCAAGCTGGAGCGGTACGCGCAAGTTCAACAAAGGGGGCTGTTAAGT	53698	QY	2574	CTGGGCGGAGTTTCATCAGCTGTGCGCGCATTTTTCGAGAGCGCGCGGATGCGCGCGCC	2633
QY	1506	GTGGACATTCGGCGAGACCACTTTCAAGACGCGAGCAAGATCAAGGTGAACGGGATGGT	1565	Db	52617	TTGGGCGACGCGCGCTGCTGGAGGACAAATTTTTCAGGGGCTATAGGTTTTCGGAACCA	52558
Db	53697	GTGGGACATCCGCAAGCAACATTTTCAAGAAAGAGCAAGGTGAATCAATGCGCTGAT	53638	QY	2634	CGGTCCTTACTCCATGCGCATCTACGGGGACACGAGCTCCATTTTTCGTTTGTGCGG	2693
QY	1566	GAAATCGACATGACGATCATCATCCGCAAGGTCAAACTCTCCAGCTACAAGCTGAA	1625	Db	52557	CAAGCTTACTCTCGCTCAGGGTTATCTACGGAGACACCGACTCCGCTTTTATCAAGTTGT	52498
Db	53637	ATCTCTAGACATGATTCTGTGGCGACGGAAGCTAAAGCTACCCAGCTACAAGCTCGA	53578	QY	2694	CGGCTTCAACCGCGCGCTGCTGGGCGCATGCGGCGCAAGATGCGGAGCCACATCTCGCG	2753
QY	1626	CGCGCTCGCGAGGCGCTTTGAAGGACAAAGAAAGGATCTGAGCTACCGCGACATCCC	1685	Db	52497	GGGCTCAGCTACGAGGGGGTATCGGAGCTGGGGGATGCTATGTGCGCTCAGATTTTCAGC	52438
Db	53577	CGCGCTCGTGGAGAGCTCTCGCGGAGCATTAAGATAGACCTTCCCTATAAAGAAATACC	53518	QY	2754	CGCGCTGTTCTTCCCGCGGCTCAAGCTCGAGTGCAGAAAAACGTTTCAACAGCTGCTGCT	2813
QY	1686	CGCTACTACGCTTCCGGGCGCGGCGAGCGCGGGGTGATCGGCGAGTATTGTGTGAGGA	1745				

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Db 52437 GGACCTCTTTAGAGCGCCCATCAAACTGGAGTGTGAGAGACCTTTTCAGCGACTGCTGCT 52378
Qy 2814 CATCGCCAGAAAAAGTACATCGCGTCTCTCGGGGGCAAGATGCTCATCAAGGCGT 2873
Db 52377 GATCACAAGAAAGATACATAGTGTGTCATAAACCGGGGGAAGATGCTCATGAAGGGGT 52318
Qy 2874 GGATCTGGTGGCAAAACAACTGCGGTTTATCAACCCGACCTCCAGGCGCTGTGTCGA 2933
Db 52317 CGACCTGGTCCGCAAAATAACTGCTCTTTCATATAACTTGTAGCGCGACATCTGTAGA 52258
Qy 2934 CCTGCTGTTTTTACGAGATACCGTATCCGGAGCGCGCGCTTACCGAGCGCCCCG 2993
Db 52257 TCTTTTGTGTACGACGAGGATGTGGCCACGCGCGCAGCAGAGGTGACAGACGTGCTCC 52198
Qy 2994 AGAGGAGTCTGGCGGACCCCTGCGCGAGGAGTCTCAGGCGTTTCGGGCGCTCTCGT 3053
Db 52197 CGCAGATGGTGGGCGCGCCGCTTACCGAGCGCTTTTGACANGTTTGGGCGAGTGTGGT 52138
Qy 3054 AGACGCCATCGCGCATACCGACCGGAGAGGACATCCAGACCTTTGTCTCACCGC 3113
Db 52137 AGAGCGTACACCGTATCACTGCGCCCACTTGGAGCTGCGGAGTTCGTTATGACTGC 52078
Qy 3114 CGAACTGAGCAGACACCGCGCGCTACACCAACAGCGCTCGGCCACCTGACGCTGA 3173
Db 52077 TGAGCTGAGCGCTCACCCGAATCGTATACCAACAGCGCTCGCGCACCTCACCGTCA 52018
Qy 3174 TTACAGCTCATGGCCCGCGCGGAGTCCCGTCCATCAAGACCGGATCCGTACGT 3233
Db 52017 CTTTAAAGCTCGCATGAGGAATGAAGAACTGCCAGCGTAAAGAGAGAATTCGTTATGT 51958
Qy 3234 GATCGTGGCCAGACCGCGAGGTAGAGGAGCGTTCGCGCGCTGGCGCCCTCCGCGA 3293
Db 51957 GATAGTTGCGAGACC-----GAGGCCGCGGNAACGGA 51925
Qy 3294 GCTAGAGCGCGCGCCCGCAGGAGAGCGCGCGCCCGCCCGAGCGCCCTGCCCTCCCGCGC 3353
Db 51924 AGCGGCTGTAGTAACTCAATGCGCGGTACCGCCCAAAACCCCGTGTGTAAACCAAGACCGC 51865
Qy 3354 CAAGCGCCCGCGGAGACGCGTTCGATCGGACCGCCCGGAGCGCGTCCAGCGCCG 3413
Db 51864 ACGCCCAACCTAA-----ACG 51847
Qy 3414 CAAGCTCTGCTGTGTCGAGTGGCGGAGGATCCGGGTAGCCCATCGCCGGCGGCGTTCC 3473
Db 51846 CAAACTGCTGTTCCGACCTCGCGAAGACCGACCTATGTTTCCGAGATGACGTACC 51787
Qy 3474 GCTCAACACGGAATTAATTTCTCGACCTGCTGGGGGGCGGCGCTGCGTGAAGTCAAGGC 3533
Db 51786 GCTAAACACAGACTACTATTCTCCCACTGTTGGGTACCATAGCGTGACCTTTAAGGC 51727
Qy 3534 CCGTTTGGAAATAACCCCAAGATCACCGAGAGTCTGTTAAGAGGTTTATTTCCCGAGAC 3593
Db 51726 TCATTTCGGAATGATGTGAAACAACAGAAATCTTTTAAAGCGGTTTATTCGGAAC 51667
Qy 3594 GTGGCAC- - -CCCCCGGACAGCTGGCGCGCGGCTCAGGCGCGCGGGTTCGGGCGCGC 3650
Db 51666 CCCCCAAGACCCCAAGAAACCCAGGCACTGCTTTGAGCGCGCGCTTTGAAAGCT 51607
Qy 3651 GGGGGCGCGGCTACCGCGGAGGAACTCGTCGATGTTGATAGACCTTTGATCTCT 3710
Db 51606 GACGCCCTTTACACCGGAGGAAGTCTGTCGAATATCTGCATACAGTTTTTTTGTACTCT 51547
Qy 3711 AGCA 3714
Db 51546 AGAA 51543
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RESULT 11
ADP74216/c
ID ADP74216 standard; DNA; 150071 BP.
XX AC
XX ADP74216;
XX

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DT 26-AUG-2004 (first entry)
XX Equine herpesvirus 1 genome gM deletion mutant #1.
DE virucide; vaccine; Equine Herpes Virus; EHV; gM; vaccine;
XX EHV-associated condition; Equine herpesvirus 1; EHV1; ds; mutant; mutein.
OS Equine herpesvirus 1.
OS Synthetic.
XX US2004109873-A1.
XX 10-JUN-2004.
XX 21-JUL-2003; 2003US-00624149.
XX 19-JUL-2002; 2002DE-01033064.
XX 14-AUG-2002; 2002US-0403282P.
XX 11-APR-2003; 2003DE-01017008.
XX (BOEH ) BOEHRINGER INGELHEIM VETMEDICA GMBH.
XX Neubauer A, Ziegler C;
XX WPI; 2004-440311/41.
XX New recombinant equine herpes (EHV) virus free of heterologous elements,
PT and where protein gM has been deleted, useful as a vaccine for treating
PT or preventing EHV infections.
XX Claim 8; Page; 156pp; English.
XX The invention describes a new recombinant Equine Herpes Virus (EHV) where
CC the protein gM is absent, and the EHV is free of heterologous elements.
CC Also described are: a nucleic acid coding for an EHV defined above; a
CC vaccine preparation comprising the EHV or nucleic acid; obtaining a
CC recombinant EHV; and a cell line for use in the method, where the gene
CC encoding the protein gM is transfected into the cell line, and the cell
CC line expresses gM. The vaccine comprising the EHV or nucleic acid
CC encoding EHV is useful for treating and/or preventing EHV-associated
CC condition, and for monitoring the therapeutic success. The recombinant
CC EHV is useful as a vaccine against EHV infections. This sequence
CC represents an Equine herpesvirus 1 genome in which nucleotides 93268-
CC 93318 and 94222-94322, comprising regions of the gM gene, have been
CC deleted.
XX Sequence 150071 BP; 32583 A; 43129 C; 41914 G; 32445 T; 0 U; 0 Other;
SQ Query Match 29.7%; Score 1104.8; DB 12; Length 150071;
Best Local Similarity 59.1%; Pred. No. 1.6e-169;
Matches 2131; Conservative 0; Mismatches 1317; Indels 156; Gaps 8;
Qy 186 GGTCTAGCGCCATACGTACTACAGCGAGTGCAGAGATTTTCGATTTATCGCCGCGTTC 245
Db 55065 GCCCCCCCAACATCTGCTACTGCACAGAGTGGGTAGCTTTTAAAGTTATAGCTCCAAGATG 55006
Qy 246 GCTGGACGAGACGCGCCCCCGGAGCAGCGCACCGGGGTCCACGACCGCGCCCTCCGCGC 305
Db 55005 CCTCGATGAGAGAGCCCCCGCCGACCGACGCGGTGTACACGTGGGACCTTGGAGCG 54946
Qy 306 CGCCCTTAAGGTGTACTGCGGGGGGACGAGCGGAGTCTCTCGGCGTGGGCCCGGAGGG 365
Db 54945 CCCACCAAAAGTGTACTGCGATGGCTCAGAGTACGACGTCTGAACCTTTGCCTCCGAGG 54886
Qy 366 CTTCTGCGCGCTCGCTTGGCGCTGTGGGCGGTGGGACCATGCCCCCAAGGGGTTCGA 425
Db 54885 TTGCTGGCTCGCAGGATTCGGGTTTGGAAACGCCAGGATTTTCGGGGCGATGATTCAA 54826
Qy 426 CCCACACCGTCAACCGTCTTCCACGTGTACGACATCTCTGGAGCAGCGTGAACACGCGTACAG 485
Db 54825 CCCAGATTTGAGAGATTTTCACGTGTACGACATAGTAGAGACTTCGGAGAGCGCCTCACA 54766
Qy 486 CATGCGCGCGCCAGCTCCACGAGCGATTTATGAGGCCATCACGCCCGCCCGGACCGT 545
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Db	54765	CGATGACCCATCCAGGTTTCTGAGCTAT-----CCCGCCCAAGCGGCTCTGT	54718	53697	GTGGGACATCGCCACGAACCACTTTTTCAGAGAAGAGCAAGGTGAATAAATCAATGGCCTGTAT	53638
Qy	546	CATCAGCTTCTGGGTTCTGACCCCGAAGGCCATCGCGTCCGCGTTTCAGCTCTACGGCAC	605	1566	GAAATCCAGATGTACGGCATATCACCAGCAAGGTCAAACTCTCCAGCTACAGCTGAA	1625
Db	54717	GGTAACACTGTCTGGGAATGAGCGAGTGTGGAAAGCGAGTCGCGGTTTTCAGCTCTATGGTGT	54658	53637	ATCTCTAGACATGATTTCTGTGGCGACGGAAGCTAAAGCTACCACTCAAACTCGA	53578
Qy	606	GGCGAGTACTTTTATCATGAACAAGCGGAGGTGGATCG-----	644	1626	CGCGTCCCGCAGGCGCTCTTTGAAGGACAAAGAAGAGATCTGAGCTTACCGCGACATCCC	1685
Db	54657	GGCCCATTTATTTATATGCAAAAGCGGAGGTGATAGCGCTTGTGGAAATAACACCGA	54598	53577	CGCGTCTGTGGAGACGTCCTCGGCGACATAAGATAGACCTTCCCTATAAGAAATACC	53518
Qy	645	-----GCACCTGCAGTCCGTCGCCCGC-----GATCTCT	676	1686	CGCCTATACGCTCCGCGCCCGCGACGCGGGGTGATCGCGAGTATTTGTGTCAGGA	1745
Db	54597	GGCAGAACTCGTGGCGCAATGGTGAAGTGCAGCTCGGCTTTGAGCGCGGCCCT	54538	53517	CTCCTATTACCGGAGGGCCTGACCGGAGGGCGTAAATAGGAGAGTATTTGATCCAGGA	53458
Qy	677	GGAGCGCTGGCGCGGCCCTTGGCGAGTGCSCGGGGCGTTCGTCGCG-----	728	1746	CTCGTCTGTCTGGGAGCTGTTCTTCAAGTTCGCGGCACCTGGAGCTTTCGCCGT	1805
Db	54537	GGGAATGGCAACGGCGGCAACAGAGCGCGGAGCGGGGATGGTGGGGCGGAAA	54478	53457	CTTAGGCTGTGGGCAAGCTGTTTTTAAAGTACCTCCCCCATCTGGAAGTATCGCGGT	53398
Qy	729	---CATCTCCGCGACCACTTCGAGCGGAGGTGGTGGAGCGCGCGCTGTACTATTA	785	1806	CGCGCGCTGGCGGGCATCAACATCACCGCACCATCTACGACGGCCAGAGATCCGCT	1865
Db	54477	GCACGTGTCTCGGACTGCTTCAAAGTGGAGACCGTGTGCCACACGACGCTACTACTT	54418	53397	GGCCAAACTCGCCGATCACCCCTAAACGGGGTAAATTTTGACGGTCAAGCAATTCGGGT	53338
Qy	786	CGAAACGGCCCGACCTGTACTACCGGTCTTCGTGCGAAGCGGGCGGCGTGGCCCTA	845	1866	CTTCACTGTCCTCTCGCGCTTGGGGCCAGAAAGGCTTCATCTGCGGACACCCAGG	1925
Db	54417	TGGATCTAAGCCAGCTCTCTACTATAGAGTATCTGCCTCCAGCAGCGCCTGGAGGTT	54358	53337	GTACACGTGCTTGTGAAACTCGCCCGCGAGAGAAATTTCAATTTTGCAGACACAGACG	53278
Qy	846	CCTGTGCGACAACTTTTGCSCCGCATCAGGAAGTACGAGGGGGCGTCCAGCCACCAC	905	1926	GCGGTTTCGGGGCTTCGACAGGAGGCGCCCAAGCGCCGCGCTGCTCGG-----	1978
Db	54357	CATCTGCGACAACTTTACCGGAGATTACAAATTCGAGGGGAGCGTGGACGACAC	54298	53277	CCGTTTGAAGTCAAGTCAGGACGCGCGTCAAGACTTTCGAGTGGGTATGGATAGCCA	53218
Qy	906	CCGTTTATCTCGGAACAACCGGGGTTTGTCACTTTCGGCTGTGTACCCGCTCAAGCCCGG	965	1979	-----GGGAAGGGAGGCGCGCGGGACGGGAACGGGACAGGATTAAGACGACGAGA	2033
Db	54297	CGGCTGTTTGGACAATGAAATTTTACCAGTTTCGGTGGTGTACCGCTCGGACCGG	54238	53217	AAGCCACGCTTCGACAGTACAGACGAAACCGACGGTGTGACGGTACCCCGGACCGCG	53158
Qy	966	CGCGGGAAACGGCGCGCCCAACCGCGCCCGGACGCGGTTTGGAACTCGAGCGACGT	1025	2034	GGAAGGAAACGGGACGAGCGGAGGAGTTCGCGGAGAGACCGGGGCGCGGACGTTGG	2093
Db	54237	CACCCACGAGAGCGTGTCAACTTCGCGCCGCTTGGAGCGACACGTCACCTCAAGCGACGT	54178	53157	AGGATCTGGCGCTACTTCTGAAACCGGAGGCGGAAGCCCGCGTTCGGGAGGCGGCTGGG	53098
Qy	1026	CGAGTTTAATCTGACGGCGGACACCTCGCGCTCGAGGGGCCATGTGTGACCTCGCGC	1085	2094	GTACAGGGGGCGCGGCTCTCGACCCCACTCGGGGTTTCACTCGACCCGCTGGTGT	2153
Db	54177	GGAGTTAACTGTACTCCGATTAACCTGGAGCGGATACAGAGGCGTGCCTGGCCCGA	54118	53097	CTACAGGAGCAAAAGTTCTAGACCCGCTATCCGGCTTTCATGTGGAACCCGCTGGTGT	53038
Qy	1086	CTAAGCTCATGTCTTCGATATCGAATGCAAGCGCGGGGGAGAGACGAGCTGGCTT	1145	2154	GTTTGACTTTGCCACGCTGTACCCAGCATCATCCAGGCCCAACCTGTCTCAGTAC	2213
Db	54117	CTATAAGCTCATGTCTTGTATAGAGTGTAAAGCTGGAAGCGGTAAAGAAATGGGCTT	54058	53037	GTTTGACTTCGCTAGCTTATACCCAGCATATACAGGCCCATAACTCTCTTTCACCA	52978
Qy	1146	TCGGTTCGGGAAACGCCCGGAAGACCTCGTCAATCCAGATCTCTGTCTGTCTACGACCT	1205	2214	GCTCTCTCGCGGCCCGAGCGCTTCGCGACCTGGAAGCGGACCGGACTACCTGGAGAT	2273
Db	54057	CCCAAGTGGCAACTAAACCAAGAGGACCTGGTCAATCCAGATCTCTGTCTGTACTCGCT	53998	52977	CCTGGCGCTCGATGAAGTGGATCTGGCGGGCTTCAACCATCCGTCGACTACTCGACGT	52918
Qy	1206	GTCCACCAACCGCTCGAGGACATCTCTCTGTTTTCGCTCGGATCCCTGACCTCCCGA	1265	2274	CGAGTGGGGCGCGCGCTGTCTTCTGTGAAGGCCCACTAGCGGAGAGCTGCTGAG	2333
Db	53997	TGCTACTGAAACACAGAACACACCTCTGTCTTCCCTCGGGTCATCGGATATCTCTGA	53938	52917	CGAGTGGGTGACCAAAAGTTATTTTGTCCAGCCCATATTCGCGAAAGGCTGCTGG	52858
Qy	1266	GTCCCACTCGAGATCTCGCTCCAGGGGCTCGCGGCCCGCTCGCTCTGGAAGTTGA	1325	2334	CATCTCTCTCGGACCTGGCTGGCCATTCGGAAGACAGATCCGCTCGGGATCCCCAGAG	2393
Db	53937	GGAATACTCGTTGATCGTCCAGCGCGCGGAGCCAGACCGAGCGTTTGGAGTTGA	53878	52857	CATCTCTCTGGCGACTGGCTGGCCATTCGGAAGCGGTCGAGGCGCGGATCCCCACAG	52798
Qy	1326	CAGCAATTCAGATGTCTGGCTTCATGACCTTTCGTCAAGCAGTACGGCCCGGAGTT	1385	2394	CACCCCGAGAGGCGCTCTCTTCGACAAAGCAAACAGCGGCCCATCAAGGTGGTGC	2453
Db	53877	CAGCGAGTACGAGTGTCTGGTGGCTTCTCAAGCAGTCTCTCAAGCAGTCTCTCCCGAGTT	53818	52797	CACCCCGAGAGGCGAGTCTTACTAGATAAGCAGCAGTCTGCGATTAAAGGTGATG	52738
Qy	1386	CGTGAACGGGTACAAATCATCACTTCACTGAGCTGCGCTTCTCTGACAGCTGACGGA	1445	2454	CTCGTGTACGGGTTCAACCGGGCGCAGCGGTCTTCTGCGCTCTGCAAGTGGCGC	2513
Db	53817	GGCACCAGCTTACAAATCATGTTAATTTTGAATGGGCGTACATAGTTAAACAGGTAA	53758	52737	CTCGGTTTACGGATTTACCGGGGTGGCAACCGGCTTCTGCGGTCTGAGGATAGCGG	52678
Qy	1446	GATCTCAAGTTCGCTCGACGGGTACGGCGCATGAACGGCGGGGTGTTTCCGCT	1505	2514	CACCGTGACACCATCGGCGCGAGATGCTCTCGGACGCGCGCTGACGCGCGG	2573
Db	53757	GGTGTAAACATCAAGCTGAGCGGTACGGCAAGTTCAAACAAAGGGGGCTGTTAAGT	53698	52677	TACCGTTACCAAGTAGGACGCGACATGCTCTCAAGACCGGAGATACGTTCACTCTG	52618
Qy	1506	GTGGACATCGGCGAGACCACTTTTCAGAAAGCGGACGAGATCAAGGTGAACGGATGGT	1565	2574	CTGGGCGAGTTCGATCAGCTGTGGCCGACTTTTCGGAGGCGGCGGATGCGCGCCC	2633
				52617	TTGGGCGACGCGGAGCTGCTGGAGGACAATTTTCCAGGGGCTATAGGTTTCCGAAACCA	52558

Qy	2634	CGGTCCGTACTCCATGCGCATCATCTACGGGACACGGA	2693
Db	52557	CAAGCCCTTACTCCGTAGGGTTATCTACGGAGACACCGA	52498
Qy	2694	CGGCTCACGGCCGGGCTGTGGCCATGCGGACAGATGG	2753
Db	52497	GGGCTTACGTACGAGGGGGTATCGGAGCTGGGGATGT	52438
Qy	2754	CGGCTGTCTCTCCCGCATCAAGTTCGAGTCGGA	2813
Db	52437	GGACCTCTTTAGAGCGCCATCAAACTGGAGTGTGAGA	52378
Qy	2814	CATGCCAAGAAAGTACATCGGCTCATCTCGGGGGCA	2873
Db	52377	GATCACCAGAAGAGTACATAGTGTGTATAAACGGGG	52318
Qy	2874	GGATCTGGTGGCAAAAAACAACTGCGGTTTATCAAC	2933
Db	52317	CGACCTGGTGGCAAAAAAATACTGCTCTTTCATAAA	52258
Qy	2934	CTGCTGTTTACGACGATACCGTATCCGAGCGCGCG	2993
Db	52257	TCITTTTGTGTACGACGAGTGTGGCCACGGCGCAG	52198
Qy	2994	AGAGGAGTGGTGGCGGACCCCTGCGGAGGACTCGA	3053
Db	52197	CGCAGAATGGTGGGGCGCCCGCTTACCGAGCGCTT	52138
Qy	3054	AGACGCCCATCGGCGCATCACCGACCGGAGAGGGA	3113
Db	52137	AGAGCGGTACAAACCGTATCACTGCCCACTGGAG	52078
Qy	3114	CGAATCGAGCAGACACCGCGCGGTATACCAACAG	3173
Db	52077	TGAGCTGAGCGCTCACCGCAATCGTATACCAACAG	52018
Qy	3174	TTACAAGCTATGGCCCGCGCGAGTCCCGTCCATCA	3233
Db	52017	CTTTAAGCTGCCATGAGGAATGAAGAACTGCCAGG	51958
Qy	3234	GATCGTGGCCAGACCCGCGAGGTAGAGAGACGGT	3293
Db	51957	GATAGTTGGCGAGACC-----GAGCGCGCGGAAC	51925
Qy	3294	GCTAGACCGCCCGCCAGGGAGCAGCCGCCCCCGC	3353
Db	51924	AGCGGGTGTAGTAAACTCAATGCGGGTACCGCCCA	51865
Qy	3354	CAAGCGCCCCGGGAGACGCGTCCGATGCGGACCC	3413
Db	51864	ACGCCCCAACCTAA-----ACG	51847
Qy	3414	CAAGCTGCTGTCCGAGCTGGCGGAGGATCCGGGTAC	3473
Db	51846	CAAACTGCTGGTTTCCGACCTCGCGGAAGACCCGA	51787
Qy	3474	GCTCAACACGACTATTACTTCTCGACCTGCTGGGG	3533
Db	51786	GCTAAACACAGACTACTATTCTCCCACTGTGGGTAC	51727
Qy	3534	CCTGTTTGGAAATAACGCCAAGATCACCGAGGTCT	3593
Db	51726	TCTATTCCGAAATGATGTGAGAAACACAGAAAAAT	51667
Qy	3594	GTGGCAC---CCCCCGGACGCTGGCGCGCGCTCAG	3650
Db	51666	CCCCCAACAAGACCCCAAGAAACCCAGGCACCTGT	51607
Qy	3651	GGGGCGCGGCTACCGCGGAGGAAACTCGTCAATGT	3710
Db	51606	GACGCCCTTTACACCGGAGGAGAAAGTGTGCGAATA	51547

Qy	3711	AGCA 3714
Db	51546	AGAA 51543
RESULT 12		
ADP74201/c		
ID	ADP74201 standard; DNA; 150223 BP.	
XX	ADP74201;	
AC		
DT	26-AUG-2004 (first entry)	
XX	Equine herpesvirus 1 genome seqid 1.	
DE		
XX	virucide; vaccine; Equine Herpes Virus; EHV; gM; vaccine;	
KW	EHV-associated condition; Equine herpesvirus 1; EHV1; ds.	
XX	Equine herpesvirus 1.	
OS		
XX	US2004109873-A1.	
PN		
XX	10-JUN-2004.	
XX	21-JUL-2003; 2003US-00624149.	
XX	19-JUL-2002; 2002DE-01033064.	
PR	14-AUG-2002; 2002US-0403282P.	
PR	11-APR-2003; 2003DE-01017008.	
XX	(BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.	
XX	Neubauer A, Ziegler C;	
XX	WPI; 2004-440311/41.	
PT	New recombinant equine herpes (EHV) virus free of heterologous elements,	
PT	and where protein gM has been deleted, useful as a vaccine for treating	
XX	or preventing EHV infections.	
PS	Disclosure; SEQ ID NO 1; 156pp; English.	
XX	The invention describes a new recombinant Equine Herpes Virus (EHV) where	
CC	the protein gM is absent, and the EHV is free of heterologous elements.	
CC	Also described are: a nucleic acid coding for an EHV defined above; a	
CC	vaccine preparation comprising the EHV or nucleic acid; obtaining a	
CC	recombinant EHV; and a cell line for use in the method, where the gene	
CC	encoding the protein gM is transfected into the cell line, and the cell	
CC	line expresses gM. The vaccine comprising the EHV or nucleic acid	
CC	encoding EHV is useful for treating and/or preventing EHV-associated	
CC	condition, and for monitoring the therapeutic success. The recombinant	
CC	EHV is useful as a vaccine against EHV infections. This sequence	
CC	represents the Equine herpesvirus 1 genome.	
XX	Sequence 150223 BP; 32615 A; 43173 C; 41953 G; 32482 T; 0 U; 0 Other;	
Query Match 29.7%; Score 1104.8; DB 12; Length 150223;		
Best Local Similarity 59.1%; Pred. No. 1.6e-169;		
Matches 2131; Conservative 0; Mismatches 1317; Indels 156; Gaps 8;		
Qy	186	GGCTCAGCGCCATACGTTACTACAGCGAGTGGCGAGAAATTCGATTTATCGCCCGCGTTC 245
Db	55065	GGCCCCCAACACTCGTACTGCACAGAGTGGGTAGCTTTAAAGTTTATAGCTCCAAGATG 55006
Qy	246	GCTGGACGAGAGCGCCCGGAGCAGCAGCGGGTCCAGCGCCCGCTCCCGCG 305
Db	55005	CCTCGATGAAGAAGCCCCCGCCAGCAGCGGTGTACACGTGGGACCTTTGGAGCG 54946
Qy	306	CGCCCTTAAGTGTACTGCGGGGGGACGAGCGGAGCTCTCCCGTGGGCCCGGAGGG 365
Db	54945	CCNACCCAAAGTGTACTGCGATGCTCAGAGTACGACGTGTGAACCTTTGCCTCCGAGG 54886
Qy	366	CTTCTGGCGCGTGTGCTTGGCCCTGTGGGGGCGGTGGGACCATGCCCCCAAGGGTTCCA 425

Db	54885	TTGCTGGCTCCAGGATTCGGGTTGGAACGGCCAGGATTTTCGGGGCGATGGATTCAA	54826	Db	53817	CGCACCGGCTCAACATCGTTAAATTTTGACTGGCGGTACATAGTTAAACAAGGTAACGTC	53758
Qy	426	CCCCACCGTCAACCGTCTTCCAGCTGTACGATCATCTGGAGCACGTGGAAACACGCGTACAG	485	Qy	1446	GATCTACAAGTCCCGCTCGACGCGGTACGGCGCATGAACGGCGGGGTGTTCGCGGT	1505
Db	54825	CCCCAGATTGAGAGATTTCAGCTGTACGACATAGTAGAGACTTCGGAGAGCGCTCACA	54766	Db	53757	GGTGTATAATCAAGCTGGACGGGTACGGCAAGTTCAACAAGGGGGGCTGTTTAAGGT	53698
Qy	486	CATGCGCGCGCCAGCTCCACGACGATTTATGGACGCCATACGCCCGCGGACCGT	545	Qy	1506	GTGGACATCGCGCAGAGCCACTTTTCAGAAAGCGCAGCAAGATCAAGGTGAACGGGATCGT	1565
Db	54765	CGATGACCCATCCAGTTTGTGAGCTAT-----CCGCCCCAAGCGGCTCTGT	54718	Db	53697	GTGGGACATCGCCACGAACCAATTTTCAGAAAGAGCAAGGTGAATAATCAATGGCCTGAT	53638
Qy	546	CATCAGCTTCTGGGTCTGACCCCGAAGGCCATCGCTGCGCGTTTACGTTCTACGGAC	605	Qy	1566	GAAATCGACATGTACGGCATCATCCGACGAAGGTCAAACTCTCCAGCTACAGCTGAA	1625
Db	54717	GGTAACATCTGTGGGAATGAGCGAGTGTGGAAGCGAGTCGCGGTTCACGTTATGGTGT	54658	Db	53637	ATCTCTAGACATGTTATTTCTGGCGACGGAAGCTAAAGCTACCCAGCTCAAACTCGA	53578
Qy	606	CGGCGAGTACTTTTACATGAACAAGCGGAGGTGATCG-----	644	Qy	1626	CGCGCTCGCCGAGGCGCTTTTGAAGGACAAGAAGAGATCTGAGCTACCGCGACATCCC	1685
Db	54657	GGCCATTTATTTTACATGGCAAGCGGAGGTGATAGCGTTGTGGAATAACACCGGA	54598	Db	53577	CGCGTCTGGGAGACGCTCTCGCGGAGCATTAAGATAGACCTTCCCTATAAAGAATAACC	53518
Qy	645	-----GCACCTGCAGTGCCTGCCCGCGC-----GATCTCT	676	Qy	1686	CGCCTACTACGCTCCGCGGCCGCGAGCGGGGTGATCGCGGAGTATTTGTGTGACGA	1745
Db	54597	GGCAGAACTCGTGGCGCAATGTTGATCTGCGCGCACAGCTCGGCTTTGAGCGCGCCT	54538	Db	53517	CTCCTATTACGCGGAGGGCTGACCGGAGGGCGTAAATAGGAGATTTTGTATCCAGGA	53458
Qy	677	CGAGCGCTCGCGCGGCCCTCGCGAGTCCGCGGGGGCGTGTTCGCGCG-----	728	Qy	1746	CTCCTCTGCTGGTGGGAGCTGTTCTCAAGTTTCTGCGGACCTTGAGGCTTTCGCGCT	1805
Db	54537	GGGAATGGCAACGGCGCAAAACAGAGCGGCGGAGCGCGGGGATGGTGGGCGGAAA	54478	Db	53457	CTCTAGGCTGTGGGCAAGCTGTTTTTAAAGTACCTCCCCCATCTGGAACCTATCGCGCT	53398
Qy	729	---CATCTCGCGGACCACTTCGAGGCGGAGGTGTGAGCGCGCGAGCTGTACTATTA	785	Qy	1806	CGCGCGCTCGCGGCGCATCAACATCACCCGACCATCTACGACGCGCAGAGATCCGCGT	1865
Db	54477	GCAGTGTCTCGGACTGCTTCAAGTGGAGACCGTGTGCCACACGAGCTGTACTT	54418	Db	53397	GGCCAACTCGCCGCTATCACCTAACCGGGTAAATTTTTCGCGGTACGAAATTCGCGT	53338
Qy	786	CGAAACGCGCCCGACCTCTACTACCGGCTCTTGTGGAAGCGGCGCGCTGGCCCTA	845	Qy	1866	CTTCACGTGCTCTCGCGCTTTCGGGCCAGAAAGGCTTTCATCTCGCGGACACCCAGG	1925
Db	54417	TGGATCTAAGCCAGCTCTTACTATAGATATCTGCCTCAGACGCGCTTGGAGGGTT	54358	Db	53337	GTACACGTGCTGTGAACTCGCGCCGGAGAGAAATTCATTTCGACAGACACAGACG	53278
Qy	846	CCTGTGCAACAATTTTTCGCGCGATCAGGAAGTACGAGGGGGCGTFCGACGCCACAC	905	Qy	1926	CGCGTTTTCGGGCTCTCGACAAAGAGGGCGCCCAAGCGCCGCGCTGCTTCGG-----	1978
Db	54357	CATCTGCGACAATTTTACCGCGGAGATTACAAAATTCAGAGGGAGCGTGGACGTGACCA	54298	Db	53277	CCGTTTTGACAGTCAGGACGACGCGCGCTCAGAGACTTCGGAGTTGGCTATGGATAGCA	53218
Qy	906	CCGTTTTTCTGGAACACCGGGTTTGTACCTTGGCTGTGTACCGCTCAAGCCCG	965	Qy	1979	-----GGGAAGGGAGCGCGCGGGGACGGGAACGGGACGAGATTAAGGACGACGACA	2033
Db	54297	CGCGCTGTGTGGAACAATGAAATTTTACCAGTTTCGGGTGGTACCGCTTCGACCCGG	54238	Db	53217	AAGCCACGCTTCAGAGTACAGACGAAACCGGACGCGTGTGACGCTACCCGCGACCGC	53158
Qy	966	CCGCGGAAACCGCGCGCCCAACCGCGCCCGACGCGCTTCGGAACCTCGACGACGT	1025	Qy	2034	GGACGAGACGGGACGAGCGCGAGGAGTTCGCGCGGAGACCGCGGGCGCGCGACGTTGG	2093
Db	54237	CACCCAGGAGCGGTGTTCACTTCGCCCGTTCGAGCGACACGTCACTCAAGGACGT	54178	Db	53157	AGGATCTGGCGTACTTCTGAARAACGAGCGCGGAAGCCCGCGCTCGGAGAGCGCGTGG	53098
Qy	1026	CGAGTTTAACTGCAAGCGGCAACCTGGCCGTCGAGGGGCCATGTGTGACCTGCCGCG	1085	Qy	2094	GTACAGGGGGCGCGGTCTCTGACCCCACTTCGCGGTTCACGTCGACCCCGTGTGGT	2153
Db	54177	GGAGATTAACTGTATCTCCCGATAACCTGGAGCCGATACCAAGAGGCTGCTGGCCCGA	54118	Db	53097	CTACAGGAGCAAAAGTTCTTAGACCCCGTATCGCGCTTTTCATGTGACCCCGTGTGT	53038
Qy	1086	CTACAAGCTCATGTCTGATATCGAATGCAAGCGCGGGGAGGACGAGCTGGCCTT	1145	Qy	2154	GTTTGACTTTGCGAGCTGTACCCAGCATATCCAGGCCCCACAACTGTGCTTCAGTAC	2213
Db	54117	CTATAAGCTCATGTCTGATATAGAGTGTAAAGCTGGAACGGGTAAACGAATGGCGTT	54058	Db	53037	GTTTGACTTCGCTAGCTTATACCAAGCATATTCAGGCCCCAATACCTCTGTGTTCCACC	52978
Qy	1146	TCCCGTCCGGAACGCGCGGAAGACCTCGTCAATCCAGATCTCTGTCTGTCTACGACCT	1205	Qy	2214	GCTCTCCCTCGCGCCCGAGCGCTGCGCGACCTTGGAGCGGACCGGACCTACCTGGAGAT	2273
Db	54057	CCGAGTGGCAACTAACCAAGAGGACCTGTGATCAAGATCTCTCTGTCTGTGCTGTGCT	53998	Db	52977	CTGGCGCTCGATGAAGTGGATCTGGCGGGCTTCAACCATCTGCTGACTACTCGACGT	52918
Qy	1206	GTCCACCAACCGCTTCGAGCACTCTCTCTGTTTTTTCGCTGGATCTCTGCACTCCCGA	1265	Qy	2274	CGAGGTGGGGCGGACGCGTGTTCCTGTAAGGCCCAAGTACGCGAGAGCTGCTGAG	2333
Db	53997	TGCTACTCAGAACACAGCAACACCTGCTGTTTTTCCCTCGGGTCATGCGATATCTCTGA	53938	Db	52917	CGAGTGGGTGACCAAAAGTTATTTTTTGTCCAGCGCCATATTCGCGAAAGCTGCTGG	52858
Qy	1266	GTCCCACTCAGGATCTCGGCTCGAGGGGCTCGCGGCCCTCGCTGCTGGAGTTGA	1325	Qy	2334	CATCTGCTCGGCACTGGCTGGCCATGCGAAGCAGATCCGCTCGCGGATCCCCCAGAG	2393
Db	53937	GGAACTACTCTGTTGATGCTGCGTCCAGCGCGGCGAGCCAGACCGAGCTTTGGAGTTGA	53878	Db	52857	CATCTGCTCGGCACTGGCTGGCCATGCGAAGCGGCTGAGGCGCGGAATCCCCCAACG	52798
Qy	1326	CAGCGAATTCAGATGCTGCTGGCTTCTATCACTTGTCAAGCAGTACGCGCCCGAGTT	1385	Qy	2394	CACCCCGAGAGCGCTCTCTCTCGACAAGCAACAGCGCGCCATCAAGGTGGTGTGCA	2453
Db	53877	CAGCGAGTACAGCTGCTGTTGCTTCTGACCTTTCTCAAGCAGTACTCTCCCGAGTT	53818	Db	52797	CACCCCGAGAGGAGCTTTTACTAGATAAGCAGCAGTCTGCGGTTAAGGTGATGCA	52738
Qy	1386	CGTACCGGGTACACATCATCAACTTCGACTGGCGCTTCTGCTGACCAAGCTGACGGA	1445	Qy	2454	CTCGGTGTACGGTTTACCGGGGCGCAGACGCTTCTGCTGCTGCTGCAAGCTGCGCGC	2513
				Db	52737	CTCGTTTACGGATTTCACGGGGGTGGCAACGGCGCTGTTGCGGTGCTGAGGATAGCGCG	52678

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QY 2514 CACCGTCACGACCATCGCGCGCGAGATGCTCCTCGCAGCAGCGCGGTACGTGACACGCGC 2573
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 52677 TACCGTTACACGATAGCAGCGGACATGCTCTCTCAAGACCCGAGATTACGTTACCTCTCG 52618
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2574 CTGGGCGGAGTTTGATCAGCTGCTGGCCGATCTTTCCGGAGGCGCGCGCATGCGCGCC 2633
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 52617 TTGGGCGACGCGGAGCTGCTGGAGGACAATTTTCCAGGGGCTATAGGTTTCCGAAACCA 52558
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2634 CGGTCCGTACTCCATGCGCATCTACGGGGAACGAGCTCCATTTTTCGTTTGTGCG 2693
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DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 3174 TTCAAGCTCATGCGCGCGCGAGTCCCGTCCATCAAGSACCGGATCCGTACGT 3233
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QY 52017 CTTTAACTCGCCATGAGGAATGAGAACTGCCAGCGTAAAGAGAGAAATTCGTTATGT 51958
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QY 51957 GATAGTTGCGCAGACC-----GAGCGCGGGAACGCA 51925
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QY 3414 CAAGCTGCTGTTGTCGAGTGGCGGAGGATCCGGGTAGCCCATCCCGGGCGGTTC 3473
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DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 51726 TCTATTCCGAAATGATGTGAGAACACAGAAATCTTTAAAGCGGTTTATTCGGAAC 51667
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 3594 GTGGCAC---CCCCCGGACGACGTGTCGCGCGCGCTCAGGCGCGCGGGTTTCGGGCGCGC 3650
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QY 3651 GGGGGCGCGCTACCGCGGAGGAAACTCGTGAATGTTGCATAGAGCCCTTTCGATACTCT 3710
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 51606 GAGCCCTTTACACCGGAGGAAAGTCTGCAATGCTGCACTGCACTACACGATGTTTGTACTCT 51547
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QY 3711 AGCA 3714
DB |||||
QY 51546 AGAA 51543
DB |||||

RESULT 13
ADJ95524
ID ADJ95524 standard; DNA; 3663 BP.
XX
AC ADJ95524;
XX
DT 06-MAY-2004 (first entry)
XX
DE Equine herpesvirus type 1 ORF30 gene sequence.
XX
KW virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;
KW Equine herpesvirus type 4; genetic marker; ORF30-ml region marker;
KW viricide; vaccine; EHV-1 strain V592 polymerase ORF30-ml region;
KW neurovirulence; herpesvirus disease; gene; ds.
XX
OS Equine herpesvirus 1.
XX
FH Key Location/Qualifiers
CDS 1..3663
FT /*tag= a
FT /product= "Equine herpesvirus type 1 ORF30 protein"
XX
PN WO2004011677-A2.
XX
PD 05-FEB-2004.
XX
PF 23-JUL-2003; 2003WO-GB003279.
XX
PR 26-JUL-2002; 2002US-0398576P.
XX
PA (ANIM-) ANIMAL HEALTH TRUST.
XX
PI Davis Poynter N, Nugent J, Birch-Machin I, Allen G;
DR WPI; 2004-143877/14.
DR P-PSDB; ADJ95525.
XX
CC Assessing the virulence of a herpesvirus isolate, useful in preventing or
CC treating herpesvirus infection, by using virulence marker corresponding
CC to an ORF30-ml region.
XX
PS Claim 34; Page 61-62; 63pp; English.
XX
CC This invention relates to a novel method of assessing the virulence of a
CC herpesvirus isolate, for example Equine herpesvirus type 1 (EHV-1) or
CC type 4 (EHV-4), which comprises using a genetic marker, especially an
CC ORF30-ml region marker. The invention may be useful for the production of
CC compounds with a virucide activity or for the development of a vaccine.
CC The method, kit and sequence of the EHV-1 strain V592 polymerase ORF30-ml
CC region are useful for assessing the virulence of a herpesvirus or
CC neurovirulence. The vaccine is useful for immunising a host against a
CC herpesvirus disease and for treating disease. The present sequence is
CC that of the ORF30 gene sequence of Equine herpesvirus 1 which is related
CC to the invention.
XX
SQ Sequence 3663 BP; 866 A; 977 C; 1042 G; 778 T; 0 U; 0 Other;

Query Match 29.6%; Score 1100; DB 12; Length 3663;
Best Local Similarity 59.0%; Pred. No. 9.4e-169;
Matches 2128; Conservative 0; Mismatches 1320; Indels 156; Gaps 8;
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QY 186 GCTCAGCGCCATACGTACTACAGGAGTGCAGCAAAATTTTCGATTTATCGCCCCCGGTTT 245
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QY 120 GCCCCCCAACTCGTACTGACAGAGTGGTAGCTTTAAAGTTTATAGCTTCCAAATG 179
Db |||||
QY 246 GTGACAGAGACGCCCCCGGAGCAGGCAACCGGGTTCAGACGCGCGCTCCGGG 305
Db |||||
QY 180 CCTGATGAAGAAGCCCCCGGACACGACGACGCGGTGTACACGTTGGGACCTTTGGAGCG 239
Db |||||
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QY 240 CCCACCAAGTGTACTGGATGGCTCAGAGTACACGCTGTGAATTTTGGCTTCGGAGG 299
Db |||||
QY 366 CTTCTGGCGCGTCTGCTTGGCGCTGTGGGGGGTGGACCATGCCCCAAAGGGGTTTCCA 425
Db |||||
QY 300 TTGCTGGCCTCGCAGATTCGGGTTTGGAAACGCGCAGGATTTTCGGGGCGATGGATTCAA 359
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QY 426 CCCACCGCTACCGCTTCTCAGCTGTACGATCTCGGAGCAGTGTGAACACGCGTACAG 485
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QY 360 CCCCAGATTTGAGAGATTTTACGCTGTACGACATAGTAGAGACTTCGGAGAGCGCTCACA 419
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QY 486 CATGCGCGCGCCAGCTCCACGAGCGATTTATGGAACGCCATCACGCCGCGCGGACCGT 545
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QY 420 CGATGACCCATCCAGGTTTGTGACTAT- - - - - CCGCCCCAAGCGGCTCTGT 467
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QY 606 CGCGGAGTACTTTTATCATGAACAAGCGGAGGTGTATCG- - - - - 644
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QY 528 CGGCCATTTATTTTACATGGAAGGGCGGAGTGTGATAGCGTGTGGAATAAACACACCGA 587
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QY 729 - - - CATCTCCGGGACACTTCGAGCGGAGGTGTGGAGCGCGCGGCTGTACTATTA 785
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QY 1068 CTATAAGCTCATGTCTTTGATATAGAGTGTAAAGCTGGAACGGGTAAAGAAATGGCGTT 1127
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QY 1128 CCCAGTGGCAACTAAACAAAGGAGACCTGGTCAATCCAGATCTCTCTGTCTGTACTCGCT 1187
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QY 1206 GTCCACCACCGCCTCGAGCACATCTCTCTCTGTTTTTCGTCGATCTCTCGACCTCCCGA 1265
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QY 1248 GGAATACTCTGTTTGCATGCGTCCAGCGCGGGAGCCAGACCGGCTTTTGGAGTTGA 1307
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QY 1608 CGCGCTCGTGGGAGACGCTCTCGCGGACATAGATAGACCTTCCCTATAAAGAAATACC 1667
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QY 2208 CTTGGCGCTCGATGAAGTGGATCTGGCGGGGCTTCAACCACTCCGCTCAACTCTGAGCTT 2267
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QY 2274 CGAGTGGGGGCGGACGGCTGTTCTTCTGTGAGGGCCACGTAACGCGAGAGCGCTGCTGAG 2333
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2268 CGAGTGGGTGACCAAAAGTTATTTTGTCTCCAGCCCATATTCGCGAAAGCCTGCTTGG 2327
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 2754 CGGCTGTTCTCCCGCCGATCAAGCTCGAGTGCAGTGCAGAAACGTTTCAACAGCTGCTGT 2813
 2748 GGACCTCTTAGAGCGCCATCAAACTGGAGTGTGAGAACCTTTTCAGCGACTGCTGT 2807
 2814 CATGCCAAGAAAGTACATCGCGCTCATCTCGGGGGCAAGATGCTCATCAAGGCGT 2873
 2808 GATCACCAGAAGATGATAGTGTCTATAAACCGGGGGAAGATGCTCATGAAGGGGT 2867
 2874 GGATCTGTCGCGAAGAACTGCGGTGTTATCAACCGCACCTCCAGGCGCTGTCGA 2933
 2868 CGACCTGTCGCGAAGAAATGCTCTTCTATAAATTTGATACGCGGACATCTGGTAGA 2927
 2934 CCGTCTGTTTACGACGATACCGGTATCCGAGCGCGCGCTTAGCGGAGCGCGCCCGC 2993
 2928 TCTTTTGTGTACGACGAGATGTGGCCACGCGGCGAGCAAGGTGACACGTCCTCC 2987
 2994 AGAGGAGTGTGCGCGACCCCTGCGCGAGGAGTGCAGCGGCTTCGGGCGCGTCTCGT 3053
 2988 CGCAGATGTTGGGCGCGCGCTTACCGAGCGGCTTTGACAAGTTTGGCGGAGTGTGTT 3047
 3054 AGAGCCCATCGGGCATCACCGACCGGAGAGGAGACATCAGGACTTTTCTCTCACCGC 3113
 3048 AGAGGCGTACAACCGGTATCATCTGCCCCCACTTGGACGTGCGGAGTTCGTTATGACTC 3107
 3114 CGAACTGAGCAGACACCGCGCGGTACACCAACAGCGCTGCGCCACCTGACGGTGA 3173
 3108 TGAGCTGAGCGCTCACCGGATCGTATACCAACAGCGCTGCGGACCTCACCGTCTA 3167
 3174 TTCAAAGCTCATGGCCCGCGCGAGGTCCCGTCCATCAAGACCGGATCCCGTACGT 3233
 3168 CTTTAAAGCTCGCCATGAGGAATGAAGAACTGCCCAGCGTAAAGAGAGAATTCGTTATG 3227
 3234 GATCGTGGCCAGACCGCGGAGTAGAGGAGACGCTGCGCGGCTGCGCGCCCTCCCGGA 3293
 3228 GATAGTTGCGCAGAC-----GAGCGCGCGAAGCCGA 3260
 3294 GCTAGACGCGCGCCCGCAGGGGACGAGCCGCGCCCGCCCGCGCGCTGCGCTCCCGCGC 3353
 3261 AGCGGTGTAGTAACCTCAATGCGGGTACGCGCCCAAAACCCCGTGTGTAACCAAGACCGC 3320
 3354 CAAGCGCCCGCGGAGACGCGTGCATGCGGACCCCGCGGAGCGCGTCCCAAGCCCGC 3413

3321 ACGCCCCCAACCTAA-----ACG 3338
 3414 CAACTGCTGCTGCTGCTGCGAGCTGCGGAGGATCCCGGTACGCCATCGCCCGGGCGTTC 3473
 3339 CAACTGCTGCTGCTGCTGCGACCTCGCGAAGACCCGACCTATGTTTCCGAGAATGACGTACC 3398
 3474 GCTCAACACGAGACTATTAATTCTTCGACCTGCTGGGGGCGGCTGCGTACGTTCAAGGC 3533
 3399 GCTAAACACAGACTACTATTTCTCCACCTGTTGGGTACCATTAAGCGTGCACCTTTAAGGC 3458
 3534 CTTGTTTGAATAACGCCAAGATCACCGAGAGTCTGTTAAAGAGGTTTATTCGCCGAGAC 3593
 3459 TCTATTTCGGAATGATGTGAGAACCAAGAAAATCTTTTAAAGCGGTTTATTCGGAAC 3518
 3594 GTGGCAC---CCGCCGACGACGCTGGCGCGCGCTCAGGGCGCGGGTTCGGCGCGGC 3650
 3519 CCCCACAAAGACCCCGAACCCAGGACCTGCTTGAGCGCGCGCTTGAAAAGCT 3578
 3651 GGGGGCGCGCTTACCGCGGAGGAAATCTCGTCAATGTTGTCATAGAGCCTTTGATCTCT 3710
 3579 GACGCCCTTTACACCGGAGGAGAAAGTGTGCAATCTGCAATCTGCTACAGTCTTTTGTACTCT 3638
 3711 AGCA 3714
 3639 AGAA 3642
 RESULT 14
 ADP74214/c
 ID ADP74214 standard; DNA; 144411 BP.
 XX
 AC ADP74214;
 DT 26-AUG-2004 (first entry)
 XX
 DE Equine herpesvirus 4 genome gM deletion mutant #2.
 XX
 KW virucide; vaccine; Equine Herpes Virus; EHV; gM; vaccine;
 KW EHV-associated condition; Equine herpesvirus 4; EHV4; ds; mutant; mutein.
 XX
 OS Equine herpesvirus 4.
 OS Synthetic.
 XX
 US2004109873-A1.
 10-JUN-2004.
 XX
 21-JUL-2003; 2003US-00624149.
 XX
 19-JUL-2002; 2002DE-01033064.
 PR 14-AUG-2002; 2002US-0403282P.
 PR 11-APR-2003; 2003DE-01017008.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
 XX
 PI Neubauer A, Ziegler C;
 XX
 WIPI; 2004-440311/41.
 XX
 New recombinant equine herpes (EHV) virus free of heterologous elements,
 PT and where protein gM has been deleted, useful as a vaccine for treating
 PT or preventing EHV infections.
 XX
 Claim 18; Page; 156pp; English.
 PS
 XX
 CC The invention describes a new recombinant Equine Herpes Virus (EHV) where
 CC the protein gM is absent, and the EHV is free of heterologous elements.
 CC Also described are: a nucleic acid coding for an EHV defined above; a
 CC vaccine preparation comprising the EHV or nucleic acid; obtaining a
 CC recombinant EHV; and a cell line for use in the method, where the gene
 CC encoding the protein gM is transfected into the cell line, and the cell
 CC line expresses gM. The vaccine comprising the EHV or nucleic acid
 CC encoding EHV is useful for treating and/or preventing EHV-associated

CC condition, and for monitoring the therapeutic success. The recombinant
CC EHV is useful as a vaccine against EHV infections. This sequence
CC represents an Equine herpesvirus 4 genome in which nucleotides 92681-
XX 93865, comprising regions of the gM gene, have been deleted.
SQ Sequence 144411 BP; 35893 A; 36645 C; 36246 G; 35627 T; 0 U; 0 Other;

Query Match 23.8%; Score 885.8; DB 12; Length 144411;
Best Local Similarity 55.2%; Pred. No. 3.9e-134;
Matches 1986; Conservative 0; Mismatches 1452; Indels 159; Gaps 7;
253 GAGGACGCCCCCGGAGCAGCGACCGGGTCCACGAGCGCGCTCCGGCGCGCCCT 312
54734 GAGATGCTCCACCGATCAGCGACGCGCTGTGCGATGTGGGAACACTTGTAGCGCACCCCA 54675
313 AAGGTGTACTGCGGGGGGACAGCGCGACGTCCTCCGCGTGGGCGCGAGGGCTTCTGG 372
54674 AAGGTGTACTGATGCGCGCAGAGTACGACGCTCTAGACTTTGAAGCTGACGGTTGCTGG 54615
373 CGCGTGGTTCGCGCTGTGGGCGGTGGGACCATGCCCCCAAGGGGTTCGACCCCAACC 432
54614 CCTCGCAGGATTCGGGGTTTGGAAACCGGCAAGATTTTCGCGGTGATGAGTTTAAACCAAGA 54555
433 GTCACCGTCTCCACGTGTACGACATCTTGGAGCAGTGGACACGCTACAGCATGCGC 492
54554 TTTGAGAGGTTTCACTGTACGACATAGTAGAGTTTGTGGAAGCGCTTCGAACGACGAC 54495
493 GCCGCCAGCTCCACGAGCGATTTATGGACGCGATCAACGCGCGCGGACCGTCAATCAG 552
54494 CGTCCGCGTTTGTGAGCTATCT-----CGCCCAAGCGGATCAGTGTGTACA 54447
553 CTTCTGGGTCTGACCCCCGAAAGGCCATCGCGTGCCTGTTACGTTACGCGACGCGGCGAG 612
54446 TTGCTGGGAATGAGCGAATGTGAAAGCGCGTAGCGGTTCACGTACGGTGTGCGCCAT 54387
613 TACTTTTACATGAACAAGCGAGGTGATCG-GCACCTGAGTGCCTGCGCCCGCGGA 671
54386 TATTTTATATGAAAGTCAAGATAGACAGAGCGTGTGGAATAACGACGGAATCCGAC 54327
672 TCTCTGAGGCGCTTGGCGGGCGCCCTGCGGAGTTCGCGGGGGCGTTCCTCGCGGAT 731
54326 CTAGTTCCGCGCATGTTGCTGCGCGCACTAACTCAGCTTTAAAGCGCGCCCTGGGAAT 54267
732 CTCGCGGACCACTTCGAGCGGAGGTGGTGGAGCGCGCCGACG-----775
54266 AGCAACGAGGAAACAAAGCGGTGGAACAGCGCGCGCTGTTGGGAGGAAAGCACGTA 54207
776 -----TGTACTATTACGAACG 792
54206 TCTCTGATGTTTAAAGTTGAACAGATATGCCACAGCGCTGTACTTTTGGATCA 54147
793 CGCCGACCCCTGTACTACCGGCTCTTCGTGGGAAGCGGGCGCGCTGCGCTACTGTGC 852
54146 AAGCAACCCCTACTACTAGGGTTTCATCCTTAGCAGTCCGCTGGCGGGTTTATCTGC 54087
853 GACAACTTTTGGCGCGCATCAGGAAGTACGAGGGGGCGGTGCGACCAACCCCGGTTT 912
54086 GATAACTTCCACCCCGGAATCACAAAATTTGAGGGAGTGTGGATGTAAACAACCGGCTC 54027
913 ATCTTGGACACCCCGGGTGTGTACCTTCGCTGGTGTACCGCTCAAGCCCGCGCGGG 972
54026 TTGTTGGACAATGAAAAATTTTACAGTTTGGGTGTACCGCTCCCGCCCGGAACCAAC 53967
973 AACCGCGCGGCCAACCCCGCGCCCCGACGCGTTTCGGAACCTCGAGGAGCTCGAGTTT 1032
53966 GGAGAGCGTGTTCACCTCGCCAGGTAGAGCGACACCTGACCTCAAGTACGTTGAAT 53907
1033 AACTGACGCGGGAACACTCGCGCTCGAGGGGGCCATGTGTGACCTGCGCGCTTACAG 1092

53906 AACTGTACTTCGGATACTTAGAGCCTCTTCGGGAAGAGCGGTCTCGCCAGACATATAAG 53847
1093 CTCATGCTCTTCGATATCGAATGCAAGCGCGGGGGAGGAGCAGCTCGCCCTTTCCGGTTC 1152
53846 CTACTGTGTTTGTATATAGAGTGTAAAGCCCGGTACCGGAACGAACACTGGCGTTTCCAGTT 53787
1153 GCGGAACCCCGGGAAGACCTCGTTCATCCAGATCTCTCTGTCTGTCTAGGACCTGTCCACC 1212
53786 GCAACTAACCAAGAAGACTTGTGTAATTCAAATTTCTCTGTCTTACTCTTTAGCAACC 53727
1213 ACCGCCCTCGAGACATCTCTCTGTGTTTTCGCTCGGATCTCTGCGACTCCCGGAGTCCAC 1272
53726 CAAAGCATGAACACACCTCTGTCTCTAGGGTCTGTGATATTTCTCAAGAAATAC 53667
1273 CTCAGCGATCTCGCTCCAGGGCGCTCGCGGCCCGCTCTCTCGAGTTTGTACAGCGAA 1332
53666 GCTTCTGCTGTGTACAAAGCGGGAACTTAGCCCAACAGTCTTGGAGTTTGTATAGCGAA 53607
1333 TTCAGATGCTGTGCTGGCTTCATGACCTTCTGTCAGCAAGTACGGCCCGGAGTTCTGTACC 1392
53606 TATGAGCTGTTGATAGCAATTTTAACTTCTCAAGCAATACTCTCCAGAGTTTCCACT 53547
1393 GGGTAAACATCATCACTTCGACTGGCCCTTCTGCTCTGACCAAGCTGACGAGATCTAC 1452
53546 GGTACAACTTGTAACTTTGACTGGGCGTACATAGTTAAACAGTTGACGCTCCGTTTAT 53487
1453 AAGTCCCGCTCGAGCGGTACGGCGCATGAACGGCGGGGTGTCTCCGGGTGTGGGAC 1512
53486 AACATAAACTTGTATGGGTACGGCAAGTTTAAACAAAGAGGGGTGTTTAAAGTCTGGGAC 53427
1513 ATCGCCAGAGCCACTTTTCAAGCGCAGCAAGATCAAGGTGAACGGATGTTGAACATC 1572
53426 ATTGCTACAAACCTTCCAAAAAAGCAAGGTAAATAATAGAGTATATCTCTG 53367
1573 GACATGATGCGCATCATCACGCAAGGTCAAATCTCTCAAGTACAAAGTGAACGCCCTG 1632
53366 GACATGATTTTCGTGGCAACAGAAAAAGCTAAACACTACCTAGCTATAAACTTTGACGCG 53307
1633 GCCGAGCGCTTTGAAGGCAAGAAAGATCTGAGTACCGGACATCCCGGCTTAC 1692
53306 GTTGAAGACGTTCTAGGTGAGCAAGATAGACCTTCCATACAAAGACATACCTTCTTAC 53247
1693 TACGCTCTCGGCGCGCGCGAGCGGGGTGATTCGCGGAGTATTTGTGTCAGGACTCTGCTG 1752
53246 TATGCAAGTGGACCAACACGAGCGGGTGTATAGAGAGTATTTGTTTACAGACTCAAGA 53187
1753 CTGTCGCGGAGCTGTTCTTCAAGTTTTCGCGCACTGAGAGTTCGCGCTGCGCGC 1812
53186 TTAGTTGGAAGCTATTTTAAAGTACCTCCACATCTGGAACCTCTCTGCTGTTGCAAG 53127
1813 CTGCGGGGACATCAACATCACCGCACCATCTACGACGCGCAGATCCGCTCTTACG 1872
53126 CTAGCCCGCATAACTTAAAGCGGGTAAATTTTGTGTCAGCAAAATTCGCGTTTACACA 53067
1873 TGCCTCTGCGCTTGGGGCCAGAAAGCGTTTCATCTGCGCGGACACCCAGGGCGGTTT 1932
53066 TGCTTGTAAACTCGCAGAGAGCGGAATTTTATTTTACAGACAAACCGACGCAATTC 53007
1933 CGGGGCTCTGCAAGAGAGGCGCCCAAGCGCCCGCGGTGCTCGGGGGGAAAGGGAGCGG 1992
53006 GACTACCATGGGAGCGTGTGTGGAAGTTTCCGAGACATCCATAAATAGTGAAGACCA 52947
1993 CCGGGGACGGAACGGGAGCGAGGATAA-----GGAACGACGAGACGAGGACG 2044
52946 GCCTTTGACAACTAACTCAGATAGTATTAATGGGAGCCCAAGATGTTATGCTCG 52887
2045 GGAACGAGCGCGAGGAGTTCGCGCGAGACCCCGG-----GGCCGCGACGTTGGGTACCA 2100
52886 TCTGCCAGTTTGGAAACAGGGGGCGGAAACCCCGCACAGGTAGATTTGGGATACCA 52827
2101 GGGGCGCGGTCCTCGACCCCACTCCGGGTTTCACTCGACCCCGGTTGTTGTTGAC 2160
52826 GGAGAAAGGTGCTAGATCTATATCGGCTTTTATGTTGACCCAGTCGTTGTTGAC 52767

CC Also described are: a nucleic acid coding for an EHV defined above; a
CC vaccine preparation comprising the EHV or nucleic acid; obtaining a
CC recombinant EHV; and a cell line for use in the method, where the gene
CC encoding the protein gm is transfected into the cell line, and the cell
CC line expresses gm. The vaccine comprising the EHV or nucleic acid
CC encoding EHV is useful for treating and/or preventing EHV-associated
CC condition, and for monitoring the therapeutic success. The recombinant
CC EHV is useful as a vaccine against EHV infections. This sequence
CC represents an Equine herpesvirus 4 genome in which nucleotides 92715-
CC 93824, comprising regions of the gm gene, have been deleted.
XX
SQ Sequence 144486 BP; 35916 A; 36662 C; 36259 G; 35649 T; 0 U; 0 Other;

Query Match 23.8%; Score 885.8; DB 12; Length 144486;
Best Local Similarity 55.2%; Pred. No. 3.9e-134;
Matches 1986; Conservative 0; Mismatches 1452; Indels 159; Gaps 7;
QY 193 CGCCATAGCTACTACAGCGAGTGCACGAATTTTCGATTTATCGCCCGCGTTCGCTGGAC 252
DB 54794 CACCACTCATACTACACCGAGGTGGGCAACTTCAAGTTTCATAGCACCAAGTGTCTTGAT 54735
QY 253 GAGGACGCCCCCGGAGCAGCGCACCGGGTCCACGACGCGCGCTCCCGCGCGCCCT 312
DB 54734 GAAGATGCTCCAAACCGATCAGGACGCGCTGTGCATGTGGAAACACTTGACGCGCACCCCA 54675
QY 313 AAGGTGTACTCGGGGGGAGCAGCGCGACGTCCTCCGCTGGGCGCGAGGGCTTCTGG 372
DB 54674 AAAGTGTACTGTGTGGCGCAGAGTACGACGCTCTAGACTTTGAAGCTGACGGTTGCTGG 54615
QY 373 CGCGTCTCGCTGTGGCGGTGCGGACGATGCTCCGCTGGGCGCGAGGGTTCGACCCAC 432
DB 54614 CCTCGCAGGATTCGGGTTTGAACCGGCAAGATTTTCGCGGTGATGAGTTTAAACCCAGA 54555
QY 433 GTCACCGCTTCCACGCTGACACATCTCGAGCAGCTGGAAACACGCTACAGATGGC 492
DB 54554 TTTGAGAGTTTACGCTGACACATAGTAGAGTTTGTGAAAGCGCTTCGAAACAGCAC 54495
QY 493 GCCGCCAGCTCCACGAGCGATTTATGGACGCCATCACGCCCGCGCGGACCGTCAACG 552
DB 54494 CCGTCCGCGTTTGTGAGCTATCT-----CGCCCAAGCGGATCAGTGGTAACA 54447
QY 553 CTTCTGGTCTGACCCCGAAGGCCATCGCTCGCGTTTACGCTTACGGCAGCGCGGAG 612
DB 54446 TTGCTGGGAATGAGCGAATGTGGAAGCGCTAGCGGTTACGTTGACGGTGTGCGCAT 54387
QY 613 TACTTTTACATGAACAAGCGGAGTGTGATCG-GCACCTGCAAGTGCCTGCCCGCGCA 671
DB 54386 TATTTTATATTTGAAGTCAAGATGACAGAGCGTGTGGAAATAACACAGCAATCCGAC 54327
QY 672 TCTCTGAGCGCCTGGCGGCGGCCCTGCGCGAGTTCGCGGGGCGTGTTCGCGGCAT 731
DB 54326 CTAGTTCCGCGCATGTTGCTGCGCGCAATACTCAGCTTTAAGCGCGCCCTCGGAAT 54267
QY 732 CTCGCGGACCACTTCGAGGCGGAGTGTGGAGCGGCGCGCAAG-----775
DB 54266 AGCAACGAGGAGAAACAAGCGGTGGAACAAGCGCGCGCTGTTGGGAGGAAAGCAGTA 54207
QY 776 -----TGTAATTTAGCAACG 792
DB 54206 TCTCCTGATTCCTTAAAGTTGAACAGATATGCCACACGACGCTGTACTTTGGATCA 54147
QY 793 CGCCCGAACCTGTACTACCGCGTCTTCGTGGAAGCGGCGCGCTGGCTACCTGTGC 852
DB 54146 AAGCCAAACCTCTACTATAGGTTTTCATCTCTAGCAGTCCCTGGCGGTTTATCTGC 54087
QY 853 GACAACTTTTCCCGCGATCAGGAAGTACGAGGGGGGCTGACGCAACACCCCGTTT 912
DB 54086 GATAAATTCACACCGGAAATCAAAAAATTTGAGGGGAGTGTGGATGTAAACAACCGCGCTC 54027
QY 913 ATCTGGACAAACCCGGGTTTGTACCTTCGCTGTGTACCGCTCAAGCCGCGCGCGG 972
DB 54026 TTGTTGGACATGAAATTTTACCAGTTTGGTGGTACCGCTCCCGCGCGGAAACCAAC 53967

QY 973 AACCGCGCGGCCAACCGCGCCCGCCCGACGCGGTTTCGGAACTTCGAGCGAGCTCGAGTTT 1032
DB 53966 GGAGAGCGTGTTCACCTGCGCCAGGTAGAGCGACACCTGACCTCAAGTGACGTTGAAAT 53907
QY 1033 AACTGCACGGGGCAACCTCGCGCTCGAGGGGGCCATGTGTGACCTCGCGGCTTACAG 1092
DB 53906 AACTGTACTTCGGATAACTTAGAGCCTCTTCCGGAAGAGGGCGTCTCGGCCAGACTATAAG 53847
QY 1093 CTCATGTCTTCGATATCGAATCGAAGCGCGGGGGAGGACGAGCTCGCTCTTCGCGT 1152
DB 53846 CTACTGTGTTTGTATATAGAGTGTAAAGCCCGGTACCGGAACGAACTCGCGTTCCAGTT 53787
QY 1153 GCGGAACGCCCGGAAGACCTCGTCCATCCAGATCTCTGTCTGTCTACGACCTGTCCACC 1212
DB 53786 GCAACTAACCAAGAAGACTTGTGTAATTCAAATTTCTGTTTCTTACTCTTTAGCAACC 53727
QY 1213 ACCGCCCTCGAGCAGCATCTCTGTTTTCGCTCGGATCTCTCGGACCTCCCGAGTCCAC 1272
DB 53726 CAAAAGCATGAACACACCTCTGTTTCTTAGGGTCTGTGATATTTCTGAAGATAC 53667
QY 1273 CTCAGCGATCTCGCTCCAGGGGCTCGCGGCCCGCTCGTCTGAGTGTGACAGCGAA 1332
DB 53666 GCTTCTGCTGTGTACAAACGCGGGAACTTAGCCCAACAGTCTTGGAGTTTGTATGCCAA 53607
QY 1333 TTCAGATGTCTGCTGGCTTTCATGACCTTCGTCAAGCAGTACGGCCCGAGTTCGTGACC 1392
DB 53606 TATGAGCTGTTGATAGCATTTTAAACATTTCTCAAGCAATACTCTCCAGAGTTTGCCACT 53547
QY 1393 GGTGTACAAATCATCACTTCGACTGGCCCTTCTCTGACCAAGCTGACGAGATCTAC 1452
DB 53546 GGTGTACAAATCATCACTTCGACTGGCCGTACATAGTTTAAACAAGTTGACGCTCGCTTAT 53487
QY 1453 AAGTCCCGCTCGACGGGTACGGCGCATGAACGGCGGGGTGTTCCCGGTGTGGAC 1512
DB 53486 AACATAAACTGTATGGGTACGGCAAGTTTAAACAAGAGGGCTGTTTAAAGGTCTGGAC 53427
QY 1513 ATCGCCGACAGCCACTTTTCAGAACGCGCAGCAAGATCAAGGTGAACGGGATCGTGAACATC 1572
DB 53426 ATTGCTACAAACCACTTCCAAAAAAGCAAGGTAAATAATGAGATGATATCTCTG 53367
QY 1573 GACATGTACGGCATCATCACGCAAGGTCAAACTCTCCAGCTACAGCTGAAACCGCTC 1632
DB 53366 GACATGTATTTCCGTTGGCAACAGAAAAGCTAAACCTACCTAGCTATAAACTTGACGCGATT 53307
QY 1633 GCGGAGCGCTTGTGAAGGCAAGAAGAAGTCTGAGCTACCGGACATCCCGCCCTAC 1692
DB 53306 GTTGAAGACGTTCTAGGTGAGCAACAGATAGACCTTCCATACAAGACATACCTTCTTAC 53247
QY 1693 TAGCCTTCCGGGCCCGCGCAGCGGGGTGATTCGGCGAGTATTTGTGTGACGAGCTCGCTG 1752
DB 53246 TATGCAAGTGGACCAACACGCGGGGTGTAATAGGAGATTTGTATTCAGACTCAAGA 53187
QY 1753 CTGCTCGGCGAGTGTCTTCAAGTTTCTGCGCACTCTGAGCTTTTCGCGCTCGCGGC 1812
DB 53186 TTAGTTGGAAGCTATTTTAAAGTACCTCCCACTCTGGAACCTCTCTGCTGTGTGCAAG 53127
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DB 53126 CTAGCCGCGATAACTTAAACGCGGTAAATTTTGTAGTGTGAGCAATTCGCGTTTACACA 53067
QY 1873 TGCTCTCGCGCTTTCGGGCGCAAGAGGCTTTCATCTCGCGGACACACCGCGGGCGGTTT 1932
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QY 1933 CGGGGCTCTGACAAAGAGGCGCCAAAGCGCCCGCTGCTCGGGGGGAGGGGAGCGG 1992
DB 53006 GACTACCATGGGACGCTGTGTGGAAGTTTCGAGACATCCATAAATAGTGAAGACCCAC 52947
QY 1993 CCGGGGACGGGAACGGGGACGAGGATAA-----GGACGACGACGAGCAGGACG 2044
DB 52946 GCCTTTGACAACTAACAACTCAGATAGTATTAATGAGGAGCCAAAGATGTTATGCTCG 52887
QY 2045 GGGACGAGCGGAGGAGGTTCGCGCGGAGACCGGG-----GGCGGCACTGTTGGGTACCAG 2100

Db 52886 TCTGCCAGTTTGGAAAACAGGGGGGAAACCCGGACAGAGTAGGATTGTGGGATACCAA 52827
Qy 2101 GGGGCCCGGCTCTCGACCCCACTCCGGGTTTCACTCGACACCCCGTGGTGGTTTGAC 2160
Db 52826 GGAGCAAGGTGCTAGATCCTATATCCGGCTTTTCATGTTGACCCAGTCTGTGTGTTGAC 52767
Qy 2161 TTTGCGAGCTGTACCCAGCAGCATCATCCAGGCCCAACAACTGTCTCAGTACGCTCTCC 2220
Db 52766 TTTGCGAGCTGTATCCAGAGCATCATCCAGGCCCAACAACTTTGTTTCAACACTTAGCC 52707
Qy 2221 CTGCGGCCAGGCGCTCGGCGCACTTGAGGCGGACCGGGACTACTCTGGAGATCGAGGTG 2280
Db 52706 CTTAATGAAGTGGATTGGCTGGGCTTCAGCCGTGTGTTGACTACTCAACGTTGAGGTG 52647
Qy 2281 GGGGGCCGACGGCTGTTCTTGTAAGGCCCACTAGCGAGAGCCTGCTGAGCATCCTG 2340
Db 52646 GGGACCAAAAGTTGTTTGTGTGACGCGCACATTCGCGAAAAGCTTGCTTGGTATTTTG 52587
Qy 2341 CTGCGGACTGGCTGGCCATGCGAAAGCAGATCCGCTCGCGGATCCGCCAGAGCACCCTC 2400
Db 52586 CTGCGGACTGGCTGGCTATGCGAAAGCTGTTAGGCGACGAATTCACAAAGTACCCCG 52527
Qy 2401 GAGGAGCCGCTCTCTCGAACAGCAACAGCGCCCATCAAGGTGGTGTGCAACTCGGTG 2460
Db 52526 GAGGAGGCGATTTTGCTAGATAGCAACAGTCTGCAATTAAGTAAATATGCAACTCAGTT 52467
Qy 2461 TAGGGTTACCGGGGCGAGCAGCGTCTTCTGCGCCCTGCTGACGTGGCGGCCACCGTG 2520
Db 52466 TAGCGATTACCGGTGTGGCAACGGAAGTGTGTCATGTCTGGAATAGCAGCCACCGTT 52407
Qy 2521 ACGACCATCGCGCGAGATGCTCTCGACGCGCGCGTACGTGACGCGCGCTGGGCG 2580
Db 52406 ACTAAATAGCCCGCAACATGCTTCTCAAAACGAGAGATTACGTTCTACTATGTTGGGCG 52347
Qy 2581 GAGTTCGATCAGCTGTGCGCGAATTTCCGGAGCGCGCGCATGCGCGCCCGCGTCCG 2640
Db 52346 ACGCGTCAGCTGTTGGAAAACAAACTTCCAGGGGCTTTAAATTTTCGCAACAAAGCCT 52287
Qy 2641 TACTCCATGGCATCATCTAGGGGACACGAGTCCATTTTCTGTTTGTGCGCGGCGCTC 2700
Db 52286 TATTCTGTCAAGTATTATTACGGAGACACCGACTCTGTATTCATCAAGTTTGTGCGGCTA 52227
Qy 2701 ACGCGCGCGGCTGTGGCGCATGAGATGGCGGACCAATCTCGCGCGCGCTG 2760
Db 52226 ACATACAGGGGTTTCAGAGCTTGGAGATTCAATGTGCGGACAGATTTAGCTGACCTT 52167
Qy 2761 TTCTCTCCCGATCAAGCTCGAGTGCAGAAAAAGTTTCAACAGCTGCTGCTCATCGCC 2820
Db 52166 TTTAAAGCACTATCAAACTAGAGTGTGAAAAAACCTTCCAGCGGCTGCTACTAATTACA 52107
Qy 2821 AAGAAAAGTACATCGCGCTCATCTCGGGGGCAAGATGCTCATCAAGGGGCTGGATCTG 2880
Db 52106 AAGAAAAGTACATAGTGTATTCAACGGGGGTATAATGTCTCATGAAGGGGGTAGACCTA 52047
Qy 2881 GTGCGCAAAACAACTCGCGCTTTATCAACGCGACCTTCCAGGGCCCTGGTTCGACCTGCTG 2940
Db 52046 GTCCGTAAATAAATACTGTGCTTCTATAAAATTCTACGCGGACATCTAGTAGATCTCTG 51987
Qy 2941 TTTTACACAGTACCGTATCCGGAGCGCGCGCGCTTTAGCCGAGCGCCCGCGCAGAGGAG 3000
Db 51986 TTGTACGACGAGGAGTAGCTACCGCGGCGGCGGGTAACTAACGTGCTCCTCAGAG 51927
Qy 3001 TGGCTGCGCGGACCCCTGCCGAGGAGTGCAGGCGTTCCGGGCGCTCCTCGTAGACGCC 3060
Db 51926 TGGGTTGGGCGCCCTTCCGAGCGGCTTTGACAAGTTTGAAGAGTGTGTGATAGAAGCT 51867
Qy 3061 CATCGGCGCATCACCGCCCGAGAGGAGCAATCCAGGACTTTGTCTCTCAGCGCGCAACTG 3120
Db 51866 TACAACGATATAACCGCACCACTTGGATGTGCGCGAGTTTGTGATGACGCTCTGAGCTT 51807
Qy 3121 AGCAGACACCGCGCGGTACACCAACAGGCGCTGGCCCACTGACGCGTGTATTACAAG 3180

Db 51806 AGCCGACCGCGGAATCATATACAAACAGCGGCTACCGCACCTCACTGTTTACTTTAAG 51747
Qy 3181 CTGATGGCCCGCGCGGAGGTCCCGTCCATCAAGGACCGGATCCCGTAGCTGATCGTG 3240
Db 51746 CTCGCTATGCGGAATGAAGAACTGCCCACTGTGAAGAGAGAAATTCGTAATGATGTT 51687
Qy 3241 GCCCAGACCGCGAGGTAGAGGAGCGGTGCGCGCTGGCCGCCCTCCCGGAGCTAGAC 3300
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Qy 3301 GCGCGCCGCCAGGAGGACGAGCCGCCGCCAGCGGCGCTGCCCCCGGCGCAAGCGC 3360
Db 51634 ----- 51635
Qy 3361 CCCCGGAGACCGCTCGCATGCGGACCCCGCGGAGGCGCGTCCAAGCCCGCAAGCTG 3420
Db 51634 -----GTACTACAAACCCCGGCCATCAAAACAACACGCGCCCCCAATCCAAACGCAAACTG 51579
Qy 3421 CTGCTGTCCGAGCTGGCGGAGATCCCGGTACGCCATCGCCCGGGGCGTTCGCGCTCAAC 3480
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Qy 3481 ACGGACTATTACTTCTCGCACCTGCTGGGGGCGGCGCTGCGTAGAGTTCAAGGCGCTGTT 3540
Db 51518 ACAGACTACTATTATTTTCCCACTGTTGGGTACGATAAGCGTAACCTTTTAAAGGCATTTATTT 51459
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Qy 3601 ---CCCGCGACACGCTGGCGCGCGCTCAGGGCGCGGGGTTTCGGGCGCGGGGGGCC 3657
Db 51398 AAGACCTCCACAAAACCCAGGAGATGTTGGAGCGCGCTGGAATTTGAAAAGSCTAACTCCC 51339
Qy 3658 GCGCGTACGCGGAGGAAACTCGTCGAAATGTTTCGATAGAGCCTTTGATATCTTAGCA 3714
Db 51338 TTTTACATCGCGGAGAGAAAGTCGTCGAATACTGCATACAGTTTGTGTTACTCTAGAA 51282

Search completed: August 6, 2005, 02:16:55
Job time : 1891 secs

1	3717	100.0	3717	4	US-09-904-065-1	Sequence 1, Appli
2	3696.2	99.4	3723	4	US-09-904-065-3	Sequence 3, Appli
3	3693	99.4	154746	4	US-09-827-688-8	Sequence 5, Appli
4	3059.8	82.3	3708	4	US-09-904-065-5	Sequence 8, Appli
5	3053.4	82.1	3708	2	US-08-680-326-29	Sequence 29, Appli
6	3053.4	82.1	3708	4	US-09-904-065-7	Sequence 9, Appli
7	3047	82.0	3708	4	US-09-904-065-9	Sequence 9, Appli
8	1116.6	30.0	1654	6	5223391-4	Patent No. 5223391
9	1116.6	30.0	1654	6	5223391-4	Patent No. 5223391
10	1005.8	27.1	1678	6	5223391-1	Patent No. 5223391
11	1005.8	27.1	1678	6	5223391-1	Patent No. 5223391
12	726.6	19.5	944	6	5223391-6	Patent No. 5223391
13	726.6	19.5	944	6	5223391-6	Patent No. 5223391
14	701.8	18.9	3585	2	US-08-680-326-28	Sequence 28, Appli
15	701.8	18.9	124884	4	US-09-661-598A-76	Sequence 76, Appli
16	701.8	18.9	124884	4	US-09-913-514-1	Sequence 1, Appli
17	697	18.8	125157	4	US-09-913-514-2	Sequence 2, Appli
18	343.6	9.2	3027	2	US-08-680-326-23	Sequence 23, Appli
19	319.4	8.6	3048	2	US-08-680-326-25	Sequence 25, Appli
20	243.6	6.6	2511	2	US-08-680-326-116	Sequence 116, App
21	242	6.5	35100	2	US-08-770-379-17	Sequence 17, Appl
22	242	6.5	35100	3	US-08-757-669A-17	Sequence 17, Appl
23	242	6.5	35100	3	US-09-230-371A-17	Sequence 17, Appl
24	169.2	4.6	3729	4	US-09-904-065-11	Sequence 11, Appl
25	164.4	4.4	3729	2	US-08-680-326-26	Sequence 26, Appl
26	164.4	4.4	229354	4	US-09-705-400-64	Sequence 64, Appl
27	140.4	3.8	3039	2	US-08-680-326-27	Sequence 27, Appl

361	Db		GAGGCGTTCTGGCCGCTCGCTTGGCGCTGTGGGGCGGTGCGACCATGTCGCCCAAGGGG	420
421	Qy		TTTGACCCCAACCGTACCGTCTTCCACGTGTACGACATCTTGAGACAGCTGGGAACAGCGG	480
421	Db		TTTGACCCCAACCGTACCGTCTTCCACGTGTACGACATCTTGAGACAGCTGGGAACAGCGG	480
481	Qy		TACAGCATGGCGCGCGCCAGCTCCACGAGCGATTTATGACGCGCATACGCGCCGCGCGG	540
481	Db		TACAGCATGGCGCGCGCCAGCTCCACGAGCGATTTATGACGCGCATACGCGCCGCGCGG	540
541	Qy		ACGGTCATACGCTTTCTGGGTGTGACCCCCGAAGGCCATCGCGTGGCCGTTCAAGTCTAC	600
541	Db		ACGGTCATACGCTTTCTGGGTGTGACCCCCGAAGGCCATCGCGTGGCCGTTCAAGTCTAC	600
601	Qy		GGCAGCGGCGAGTACTTTTATCATGAACAAGCGGAGGTGGATCGGCACCTGCAGTCCCGT	660
601	Db		GGCAGCGGCGAGTACTTTTATCATGAACAAGCGGAGGTGGATCGGCACCTGCAGTCCCGT	660
661	Qy		GCCCGCGCGCATCTCTCGAGCGCCTGGCGCGGCCCTGCGCAGTCCGCGGGGGCGTCCG	720
661	Db		GCCCGCGCGCATCTCTCGAGCGCCTGGCGCGGCCCTGCGCAGTCCGCGGGGGCGTCCG	720
721	Qy		TTTCGCGGCATCTCCGCGGACCACTTCGAGCGGAGGTGTGTGAGCGCCGCGACGTGTAC	780
721	Db		TTTCGCGGCATCTCCGCGGACCACTTCGAGCGGAGGTGTGTGAGCGCCGCGACGTGTAC	780
781	Qy		TATTTACGAAGCGGCCGACCTGTACTACCGCGTCTTCTGTGCGAAGCGGGCGCGCGCTG	840
781	Db		TATTTACGAAGCGGCCGACCTGTACTACCGCGTCTTCTGTGCGAAGCGGGCGCGCGCTG	840
841	Qy		GCCTACCTGTGCGACAACTTTTGCCCGCGCATCAGGAAGTACGAGGGGGCGCTCGACGCC	900
841	Db		GCCTACCTGTGCGACAACTTTTGCCCGCGCATCAGGAAGTACGAGGGGGCGCTCGACGCC	900
901	Qy		ACCAACCGGTTTATCTGTGGAACAACCGGGGTTGTCACTTCGGCTGGTACCCGCTCAAG	960
901	Db		ACCAACCGGTTTATCTGTGGAACAACCGGGGTTGTCACTTCGGCTGGTACCCGCTCAAG	960
961	Qy		CCGGCGCGGGGAACGCGCGGCCCAACCGGCCCGCCCGACGGGTTCGGAACCTCGAGC	1020
961	Db		CCGGCGCGGGGAACGCGCGGCCCAACCGGCCCGCCCGACGGGTTCGGAACCTCGAGC	1020
1021	Qy		GACGTGAGTTTAACTGCACGGCGGACAACTGGCCGTGAGGGGGCCATGTGTGACCTG	1080
1021	Db		GACGTGAGTTTAACTGCACGGCGGACAACTGGCCGTGAGGGGGCCATGTGTGACCTG	1080
1081	Qy		CCGCGCTACAAGTCTATGTCTTCGATATCGAATGCAAGCCGCGGGGGAGGACGAGCTG	1140
1081	Db		CCGCGCTACAAGTCTATGTCTTCGATATCGAATGCAAGCCGCGGGGGAGGACGAGCTG	1140
1141	Qy		GCCTTTCGGTTCGGGAACCGCGCGGACAACTGTCATTCAGATCTCTCTGTCTGCTCTAC	1200
1141	Db		GCCTTTCGGTTCGGGAACCGCGCGGACAACTGTCATTCAGATCTCTCTGTCTGCTCTAC	1200
1201	Qy		GACCTGTCCACACCGCCCTCGAGCACATCTCTCTGTTTTCGCTCGGATCCTCGGACCTC	1260
1201	Db		GACCTGTCCACACCGCCCTCGAGCACATCTCTCTGTTTTCGCTCGGATCCTCGGACCTC	1260
1261	Qy		CCGAGTCCCACTCAGCGATCTCGCCTCCAGGGGCTCGCGGCCCGCGCTCGCTCTGGAG	1320
1261	Db		CCGAGTCCCACTCAGCGATCTCGCCTCCAGGGGCTCGCGGCCCGCGCTCGCTCTGGAG	1320
1321	Qy		TTTGACAGCGAATTTCGAGATGCTCTGGCCTTCAATGACCTTGTCAAGCAGTACGGCCCC	1380
1321	Db		TTTGACAGCGAATTTCGAGATGCTCTGGCCTTCAATGACCTTGTCAAGCAGTACGGCCCC	1380
1381	Qy		GAGTTCTGTGACCGGGTACAAATCATCAACTTTCGACTGGCCCTTCGTCCTGACCAAGCTG	1440
1381	Db		GAGTTCTGTGACCGGGTACAAATCATCAACTTTCGACTGGCCCTTCGTCCTGACCAAGCTG	1440
1441	Qy		ACGAGATCTACAAGGTTCCGCTCGACGGGTACGGGCGGCATGAACGCGCGGGGTGTGTTC	1500

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QY 2581 GAGTTTCATCAGTGTGTCGCGCACTTTCGAGGCGCGCCGCGCATGCGCGCCCGCGTCCG 2640
Db 2581 GAGTTTCATCAGTGTGTCGCGCACTTTCGAGGCGCGCCGCGCATGCGCGCCCGCGTCCG 2640
QY 2641 TACTCCATGCGCATCATCTACGGGGACACGGAATCCATTTTGTGTTGTCGCGCGGCTC 2700
Db 2641 TACTCCATGCGCATCATCTACGGGGACACGGAATCCATTTTGTGTTGTCGCGCGGCTC 2700
QY 2701 ACGGCCGCGGCTGTGTCGCGCATGCGGCAAGATGCGGAGCCACATCTCGCGCGGCTG 2760
Db 2701 ACGGCCGCGGCTGTGTCGCGCATGCGGCAAGATGCGGAGCCACATCTCGCGCGGCTG 2760
QY 2761 TTCTCTCCCGCATCAAGCTCGAGTGCAGAAAAAGTTTCAACCAAGTGTCTGCTCATCGCC 2820
Db 2761 TTCTCTCCCGCATCAAGCTCGAGTGCAGAAAAAGTTTCAACCAAGTGTCTGCTCATCGCC 2820
QY 2821 AAGAAAAAGTACATCGCGGTATCTGCGGGGCAAGATGCTCATCAAGGCGTGGATCTG 2880
Db 2821 AAGAAAAAGTACATCGCGGTATCTGCGGGGCAAGATGCTCATCAAGGCGTGGATCTG 2880
QY 2881 GTGCGAAAAAACAATGCGGCTTTTATCAACCGCACCTTCCAGGGCCCTGTGTCGACCTGCTG 2940
Db 2881 GTGCGAAAAAACAATGCGGCTTTTATCAACCGCACCTTCCAGGGCCCTGTGTCGACCTGCTG 2940
QY 2941 TTTTACGACATACCGTATCCGAGGCGCGCGCGTGTAGCCGAGCGCCCGCAGAGGAG 3000
Db 2941 TTTTACGACATACCGTATCCGAGGCGCGCGCGTGTAGCCGAGCGCCCGCAGAGGAG 3000
QY 3001 TGCGTGGCGGACCCCTGCGCGAGGAGTACGAGGCTTGGGGCGCTCTCTGCTAGACGCG 3060
Db 3001 TGCGTGGCGGACCCCTGCGCGAGGAGTACGAGGCTTGGGGCGCTCTCTGCTAGACGCG 3060
QY 3061 CATCGCGCATCACGACCGGAGAGGACATCCAGGACTTGTCTCTCAACCGCGGAGCTG 3120
Db 3061 CATCGCGCATCACGACCGGAGAGGACATCCAGGACTTGTCTCTCAACCGCGGAGCTG 3120
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Db 3181 CTATGCGCGCGCGCGAGTCTCCGTTCATCAAGGACGCGATCCCGTACGTCGTCGTG 3240
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Db 3241 GCCCAGACCGCGAGGTAGAGGAGACGTCGCGGCGTGGCGCGCTTCCGCGAGCTAGAC 3300
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Db 3301 GCCCGCGCGCGCGAGGACGAGCCCGCGCCCGCAGCGCGCTTCCCGCGGCAAGCGC 3360
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Db 3361 CCCCGGAGACGCGTTCGATGTCGACCCCGCGGAGCGCGTCCAAAGCCCGCAGAGTGTG 3420
QY 3421 CTGCTGTTCGAGCTGCGGAGGATCCCGGTACGCCATCGCCGGGCGTTCGCTCAAC 3480
Db 3421 CTGCTGTTCGAGCTGCGGAGGATCCCGGTACGCCATCGCCGGGCGTTCGCTCAAC 3480
QY 3481 ACAGCATTTACTTCTCGACCTGCTGGGGCGGCGCTGCGTTCAGGGCCCTGTGTT 3540
Db 3481 ACAGCATTTACTTCTCGACCTGCTGGGGCGGCGCTGCGTTCAGGGCCCTGTGTT 3540
QY 3541 GGAATAACGCCAAGATCAACGAGAGTCTGTTAAAGAGTGTATTCCCGAGAGCTGGCAC 3600
Db 3541 GGAATAACGCCAAGATCAACGAGAGTCTGTTAAAGAGTGTATTCCCGAGAGCTGGCAC 3600
QY 3601 CCCCCGAGACGAGTGGCGCGGCTCAGGGCCCGGGGTTCCGGCGGGGGGGGGCG 3660
Db 3601 CCCCCGAGACGAGTGGCGCGGCTCAGGGCCCGGGGTTCCGGCGGGGGGGGGCG 3660
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QY 3661 GCTACCGCGGAGAAACTCGTCCGAATGTTGCATAGAGCCCTTTGATACCTTAGCATGA 3717
Db 3661 GCTACCGCGGAGAAACTCGTCCGAATGTTGCATAGAGCCCTTTGATACCTTAGCATGA 3717
RESULT 2
US-09-904-065-3
; Sequence 3, Application US/09904065
; Patent No. 6682892
; GENERAL INFORMATION:
; APPLICANT: Homa, Fred
; APPLICANT: Wathen, Michael
; APPLICANT: Hopkins, Todd
; APPLICANT: Thomsen, Darrell
; TITLE OF INVENTION: A Method for Treating Herpes Virus
; FILE REFERENCE: 00221
; CURRENT APPLICATION NUMBER: US/09/904,065
; CURRENT FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 3723
; TYPE: DNA
; ORGANISM: herpes simplex
US-09-904-065-3
Query Match 99.4%; Score 3696.2; DB 4; Length 3723;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3714; Conservative 0; Mismatches 3; Indels 6; Gaps 1;
QY 1 ATGTTTGTGTCGCGCGCGCGCGCGCTTCCCGCGGGGAAAGTCGCGCGCTCGGGGGCG 60
Db 1 ATGTTTGTGTCGCGCGCGCGCGCGCTTCCCGCGGGGAAAGTCGCGCGCTCGGGGGCG 60
QY 61 TCTGGGTTTTTTCGCCCCCAACACCCCGGGAGGACCAACCGAGCGGACCGCGCGCTTGC 120
Db 61 TCTGGGTTTTTTCGCCCCCAACACCCCGGGAGGACCAACCGAGCGGACCGCGCGCTTGC 120
QY 121 CCGCGGACAGCTTCTACAAACCCCACTCGCTCAGACCGGAGACGAGCCAAAGGCCCC 180
Db 121 CCGCGGACAGCTTCTACAAACCCCACTCGCTCAGACCGGAGACGAGCCAAAGGCCCC 180
QY 181 GGGCGCGCTCAGCGCCCATACGTACTACAGCGAGTGCAGCAATTTTCGATTTATCGCCCC 240
Db 181 GGGCGCGCTCAGCGCCCATACGTACTACAGCGAGTGCAGCAATTTTCGATTTATCGCCCC 240
QY 241 CGTTGCTCGAGACGAGACCGCCCGCGGAGACGCGCACCGGGTCCACGACGCGCGCTC 300
Db 241 CGTTGCTCGAGACGAGACCGCCCGCGGAGACGCGCACCGGGTCCACGACGCGCGCTC 300
QY 301 CCGCGCGCCCTTAAGGTGTACTGCGGGGGGAGCGAGCGGAGCGTCTCCGCGTGGGCGCG 360
Db 301 CCGCGCGCCCTTAAGGTGTACTGCGGGGGGAGCGAGCGGAGCGTCTCCGCGTGGGCGCG 360
QY 361 GAGGGCTTCTGCGCGCGCTGCTTGGCGCTTGGCGCGTGCAGACCATGCCCCCAAGGG 420
Db 361 GAGGGCTTCTGCGCGCGCTGCTTGGCGCTTGGCGCGTGCAGACCATGCCCCCAAGGG 420
QY 421 TTGAGCCCCACCGTCAACCGTCTTCAACGTGTAGCATCTCTGGAGACAGTGGAAACGCG 480
Db 421 TTGAGCCCCACCGTCAACCGTCTTCAACGTGTAGCATCTCTGGAGACAGTGGAAACGCG 480
QY 481 TACAGATCGCGCGCGCCAGCTCCACGAGCGATTTATGAGCGCCATACGCCCGCGCGG 540
Db 481 TACAGATCGCGCGCGCCAGCTCCACGAGCGATTTATGAGCGCCATACGCCCGCGCGG 540
QY 541 ACCGTCATCAACGCTTCTGGGTCTGAGCCCCGAGGCGCATCGGCTCGCGTTACGCTTAC 600
Db 541 ACCGTCATCAACGCTTCTGGGTCTGAGCCCCGAGGCGCATCGGCTCGCGTTACGCTTAC 600
QY 601 GGCACGCGGAGTACTTTTATCATGAACAAGGCGGAGGTGGATCGGCACTTCAGTGCCTG 660
Db 601 GGCACGCGGAGTACTTTTATCATGAACAAGGCGGAGGTGGATCGGCACTTCAGTGCCTG 660
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QY	661	GCCCGCGCGATCTCTGCGAGCGCCTTGGCGGCGGCCCTGCGCGAGTGGCGGGGGGCTCG	720	QY	1741	CAGGACTCGCTGCTGGTGGGGCAGCTGTTCTTCAAGTTTCTGCGCGACCTGAGCTTTCC	1800
DB	661		720	DB	1741		1800
QY	721	TTCCGCGGATCTCGCGGACACATTCAGAGGCGGAGGTGGTGGAGCGGCCACGCTGTAC	780	QY	1801	GCGGTGCGCGCCTGGCGGGCATCAACATCACCCGACATCTACGACGGCCAGCAGATC	1860
DB	721		780	DB	1801		1860
QY	781	TATTAGAAACCGGCCACCTGTACTACCGCGTCTTCGTGCGAAGCGGGCGCGCTG	840	QY	1861	CQCGTCTTCACTGCTCTCGCTTGGGGCAGAGGGCTTCACTCTGCGGACACC	1920
DB	781		840	DB	1861		1920
QY	841	GCTTACTGTGCGACAACTTTTGGCCCGCGATCAGAAAGTACGAGGGGGCGTTCGACGCC	900	QY	1921	CAGGGCGGTTCGSGGCTCGAAGAGGGCCCAAGCGCCCGCGCTGCGGGG	1980
DB	841		900	DB	1921		1980
QY	901	ACCACCGGTTATCTTGACAAACCGGGGTTTGTACCTTCGGCTGGTACCGCTCAAG	960	QY	1981	GAAAGGAGCGCGCGGGGACGGGAAACGGGACGAGGATTAAGACGACGACGA-----G	2034
DB	901		960	DB	1981		2034
QY	961	CCGCGCGCGGAAACCGCGCGCCCAACCGCGCCCGCGACCGCGTTCGGAACCTCGAGC	1020	QY	2035	GACGAGGACGGGACGAGCGAGAGTCCGCGCGAGACCGGGGGCGGCACTGTTGG	2094
DB	961		1020	DB	2041	GACGAGGACGGGACGAGCGAGAGTCCGCGCGAGACCGGGGGCGGCACTGTTGG	2100
QY	1021	GAGCTGAGTTAACTGCAAGCGCGCAACCTTGGCGCTCGAGGGGGCCATGTGTACCTG	1080	QY	2095	TACGAGGGGGCGCGGCTCTCGACCCACCTCCGGGTTTCACTCGACCCCGTGGTGTG	2154
DB	1021		1080	DB	2101	TACGAGGGGGCGCGGCTCTCGACCCACCTCCGGGTTTCACTCGACCCCGTGGTGTG	2160
QY	1081	CGGGCTACAAGCTCATGTCTTCGATATCGAATCGAAGCGGGGAGGACGAGCTG	1140	QY	2155	TTTGACTTTGCGAGCTGTACCCAGCATCATTCAGAGGCCCAACCTGTCTTCACTAGC	2214
DB	1081		1140	DB	2161	TTTGACTTTGCGAGCTGTACCCAGCATCATTCAGAGGCCCAACCTGTCTTCACTAGC	2220
QY	1141	GCTTTCCGGTCCGGAACCGCCGGAAGACCTCGTCATCCAGATCTCTGTCTGTCTTAC	1200	QY	2215	CTCTCCCTGCGGCGCGAGGCGTCCGCACTTGAGAGCGGACCGGGACCTACTGAGATC	2274
DB	1141		1200	DB	2221	CTCTCCCTGCGGCGCGAGGCGTCCGCACTTGAGAGCGGACCGGGACCTACTGAGATC	2280
QY	1201	GACCTGTCCACACCGCCCTCGAGACATCTCTGTTTTCGCTGGATCTTGGACCTC	1260	QY	2275	GAGGTGGGGGCGCGAGGCTGTTCTTCTGAGGCGCCACGTCAGGAGAGGCTGCTGAGC	2334
DB	1201		1260	DB	2281	GAGGTGGGGGCGCGAGGCTGTTCTTCTGAGGCGCCACGTCAGGAGAGGCTGCTGAGC	2340
QY	1261	CCGAGTCCACCTCAGCGATCTCGCTCCAGGGGCTGCGGCGCCCGTCTCTGGAG	1320	QY	2335	ATCTCTGCTGCGGATGCTGCTGCGAAGCAGATCCGCTCGCGGATCCCGCAGAGC	2394
DB	1261		1320	DB	2341	ATCTCTGCTGCGGATGCTGCTGCGAAGCAGATCCGCTCGCGGATCCCGCAGAGC	2400
QY	1321	TTTGAACGCAATTCAGATGCTGTGCGCTTCATGACCTTCGTCAAGCAGTACGGCCCC	1380	QY	2395	ACCCCGGAGGAGGCGCTCTCTCGAAGCAACGAGCGCCCATCAAGGTGTGTGCAAC	2454
DB	1321		1380	DB	2401	CCCCCGGAGGAGGCGCTCTCTCGAAGCAACGAGCGCCCATCAAGGTGTGTGCAAC	2460
QY	1381	GAGTTGCGTACCGGGTACAAATCATCACTTTCGATGCGCCCTTCGTCTGACCAAGCTG	1440	QY	2455	TCGGTGTACGGGTTACACGGGGCGCGAGCATCGTCTTCTGCGCTGCTGACGTTGCGCGC	2514
DB	1381		1440	DB	2461	TCGGTGTACGGGTTACACGGGGCGCGAGCATCGTCTTCTGCGCTGCTGACGTTGCGCGC	2520
QY	1441	ACGGAGATCTACAAGGTCCCGTTCGACGGGTACGGCGCATCAACGGGGGCTGTGTTT	1500	QY	2515	ACCGTGAACGACCATCGGCGCGAGATGCTCTCTCGAGCGCGCGGTAGCTGACGCGCGC	2574
DB	1441		1500	DB	2521	ACCGTGAACGACCATCGGCGCGAGATGCTCTCTCGAGCGCGCGGTAGCTGACGCGCGC	2580
QY	1501	CQCGTGTGGACATCGGCGAGGCCCTTTTGAAGAGCGCGAGCAAGATCAAGGTGAACGGG	1560	QY	2575	TGGGCGGAGTTTCGATCAGCTGCTGCGGCTCTTTCGAGGCGCGCGGATGCGCGCGCC	2634
DB	1501		1560	DB	2581	TGGGCGGAGTTTCGATCAGCTGCTGCGGCTCTTTCGAGGCGCGCGGATGCGCGCGCC	2640
QY	1561	ATGGTGAACATGACATGTCGGCATCATACCGACAGGTCAAACTCTCCAGCTACAAAG	1620	QY	2635	GCTCCGTACTCCATGCGCATCATCTACGGGACACGGACTCCATTTTCTGTTGTGCGC	2694
DB	1561		1620	DB	2641	GCTCCGTACTCCATGCGCATCATCTACGGGACACGGACTCCATTTTCTGTTGTGCGC	2700
QY	1621	CTGAACCGCGTCCGCGAGCGCTTTGAAGGACAAAGAGGATCTGAGCTACCGCGAC	1680	QY	2695	GCTCCGTACTCCATGCGCATCATCTACGGGACACGGACTCCATTTTCTGTTGTGCGC	2754
DB	1621		1680	DB	2701	GCTCCGTACTCCATGCGCATCATCTACGGGACACGGACTCCATTTTCTGTTGTGCGC	2760
QY	1681	ATCCCGCTACTACGCTTCCGGGCGCGCGAGCGGGGTGATCGGCGAGTATTTGTG	1740	QY	2755	GCTCCGTACTCCATGCGCATCATCTACGGGACACGGACTCCATTTTCTGTTGTGCGC	2814
DB	1681		1740	DB	2761	GCTCCGTACTCCATGCGCATCATCTACGGGACACGGACTCCATTTTCTGTTGTGCGC	2820
				QY	2815	ATCCCGCTACTACGCTTCCGGGCGCGCGAGCGGGGTGATCGGCGAGTATTTGTG	2874

Db	2821	ATCGCCAAAGAAAAAGTACATCGGCGTCACTCGCGGGGCAAGATGCCTCATCAAGGGCGGT	2880
Qy	2875	GATCTGTTGGCGCAAAAAAACAACCTGCGCGTTTATCAACCGCACCTTCCAGGGGCCCTGGTGCAC	2934
Db	2881	GATCTGTTGGCGCAAAAAAACAACCTGCGCGTTTATCAACCGCACCTTCCAGGGGCCCTGGTGCAC	2940
Qy	2935	CTGCTGTTTACGACGATACCGTATCCGAGCGCGCGCGGTTAGCCGAGCGCCCGCA	2994
Db	2941	CTGCTGTTTACGACGATACCGTATCCGAGCGCGCGCGGTTAGCCGAGCGCCCGCA	3000
Qy	2995	GAGGAGTGGCTGGCGCGACCCCTGCCCGCAGGGAATGCAAGCGTTTCGGGGCGCTCCTCGTA	3054
Db	3001	GAGGAGTGGCTGGCGCGACCCCTGCCCGCAGGGAATGCAAGCGTTTCGGGGCGCTCCTCGTA	3060
Qy	3055	GACCCCATCGCGCGCATACCGACCCCGAGAGGACATTCAGGACTTTGTCTCTCAACGCC	3114
Db	3061	GACCCCATCGCGCGCATACCGACCCCGAGAGGACATTCAGGACTTTGTCTCTCACGCC	3120
Qy	3115	GAATGAGCAGACACCCCGCGGTAACCAACAAGCGCTTGCGCCACCTGACGGTGTAT	3174
Db	3121	GAATGAGCAGACACCCCGCGGTAACCAACAAGCGCTTGCGCCACCTGACGGTGTAT	3180
Qy	3175	TACAAGCTCATGGCCCGCGCGCAGGTCCCGTCCATCAAGGACCGGAATCCCGTAGCTG	3234
Db	3181	TACAAGCTCATGGCCCGCGCGCAGGTCCCGTCCATCAAGGACCGGAATCCCGTAGCTG	3240
Qy	3235	ATGTTGCCCAGACCCCGGAGGTAGAGGACGGTTCGCGGCTTGGCCGCCCTCCGCGAG	3294
Db	3241	ATGTTGCCCAGACCCCGGAGGTAGAGGACGGTTCGCGGCTTGGCCGCCCTCCGCGAG	3300
Qy	3295	CTAGACGCCGCCCGCCAGGGGACGACCGCCCGCCCGCGCGCTTGCCTCCCGGCC	3354
Db	3301	CTAGACGCCGCCCGCCAGGGGACGACCGCCCGCCCGCGCGCTTGCCTCCCGGCC	3360
Qy	3355	AAGCGCCCCGGGAGACCGCTCGCATGCGGACCCCGCGGAGCGGTCGAAGCCCCCG	3414
Db	3361	AAGCGCCCCGGGAGACCGCTCGCATGCGGACCCCGCGGAGCGGTCGAAGCCCCCG	3420
Qy	3415	AAGCTGTTGTTGTCGAGCTGGCGGAGGATCCGGGTACGCCATCGCCCGGGGCGTTCG	3474
Db	3421	AAGCTGTTGTTGTCGAGCTGGCGGAGGATCCGGGTACGCCATCGCCCGGGGCGTTCG	3480
Qy	3475	CTCAACACGACTATTACTTCTCGCACTGCTGGGGCGGCTCGGTGACGTTCAAGGCC	3534
Db	3481	CTCAACACGACTATTACTTCTCGCACTGCTGGGGCGGCTCGGTGACGTTCAAGGCC	3540
Qy	3535	CTGTTTGGAAATAACGCAAGATCACCGAGAGTCTGTTAAAGAGGTTTATTCGCCGAGC	3594
Db	3541	CTGTTTGGAAATAACGCAAGATCACCGAGAGTCTGTTAAAGAGGTTTATTCGCCGAGC	3600
Qy	3595	TGCGACCCCGGAGACGTTGGCGCGGCTCAGGGCCGCGGGGTTTCGGGCGCGGGG	3654
Db	3601	TGGACCCCGGAGACGTTGGCGCGGCTCAGGGCCGCGGGGTTTCGGGCGCGGGG	3660
Qy	3655	GCGGGGCTACGGCGGAGGAAATCTGTCGAATGTTGCATAGACCTTTGATATCTTAGCA	3714
Db	3661	GCGGGGCTACGGCGGAGGAAATCTGTCGAATGTTGCATAGACCTTTGATATCTTAGCA	3720
Qy	3715	TGA 3717	
Db	3721	TGA 3723	

RESULT 3

US-09-827-688-8	Qy	721	TTCGCGGCATCTCCGCGGACCACTTCGAGCGGAGGTGTTGAGCGCGCGCGACGTGTAC	780
; Sequence 8, Application US/09827688	Db	63985	TTCGCGGCATCTCCGCGGACCACTTCGAGCGGAGGTGTTGAGCGCGCGCGACGTGTAC	64044
; Patent No. 6821955	Qy	781	TATTACGAACGCGCGCCGACCCCTGTACTACCGCGTCTTCTGTGCGAAGCGGCGCGCGCTG	840
; GENERAL INFORMATION:	Db	64045	TATTACGAACGCGCGCCGACCCCTGTACTACCGCGTCTTCTGTGCGAAGCGGCGCGCGCTG	64104
; APPLICANT: ORSON, FRANK				
; APPLICANT: KINSEY, BERNA				
; APPLICANT: BHOGAL, BALBIR				
; TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION D				

QY	841	GCCTACCTGTGCGACAACATTTTCCCGCGCATCAGGAAGTACGAGGGGGGGGTGCGACGCC	900
Db	64105	GCCTACCTGTGCGACAACATTTTCCCGCGCATCAGGAAGTACGAGGGGGGGGTGCGACGCC	64164
QY	901	ACCACCGGTTTATCTCTGGACAACCCGGGGTGTGTCACTTCGGCTTGSTTACCGCTCAAG	960
Db	64165	ACCACCGGTTTATCTCTGGACAACCCGGGGTGTGTCACTTCGGCTTGSTTACCGCTCAAG	64224
QY	961	CCCGGCGCGGGAAACGCGCGCGGCCAACCGCGCCCCCGCAACGCGGTTTCGGAACCTCGAGC	1020
Db	64225	CCCGGCGCGGGAAACGCGCGCGGCCAACCGCGCCCCCGCAACGCGGTTTCGGAACCTCGAGC	64284
QY	1021	GAGCTCGAGTTTAACTGCAAGCGGGACAACTCGGCGGTGCGAGGGGCGCATGTGTACCTG	1080
Db	64285	GAGCTCGAGTTTAACTGCAAGCGGGACAACTCGGCGGTGCGAGGGGCGCATGTGTACCTG	64344
QY	1081	CCGGCTTACAAGCTCATGTGCTTCGATATCGAATGCAAGCGGGGGGGAGGACGAGCTG	1140
Db	64345	CCGGCTTACAAGCTCATGTGCTTCGATATCGAATGCAAGCGGGGGGGAGGACGAGCTG	64404
QY	1141	GCCTTTCCGGTTCGGGAAACCGCCGGGAGACCTCGTTCATCCAGATCTCTGTCTGTCTAC	1200
Db	64405	GCCTTTCCGGTTCGGGAAACCGCCGGGAGACCTCGTTCATCCAGATCTCTGTCTGTCTAC	64464
QY	1201	GACCTGTCCACCAACCGCCCTCGAGCAATCTCTCTGTTTTCGGCTCGGATCCTGCGACCTC	1260
Db	64465	GACCTGTCCACCAACCGCCCTCGAGCAATCTCTCTGTTTTCGGCTCGGATCCTGCGACCTC	64524
QY	1261	CCGAGTCCCACTCAGCGATCTCGCTCCAGGGGCGTCGCGGCCCGCTGCTCTGTCTGTGAG	1320
Db	64525	CCGAGTCCCACTCAGCGATCTCGCTCCAGGGGCGTCGCGGCCCGCTGCTCTGTCTGTGAG	64584
QY	1321	TTTGAACAGCAATTCGAGATGCTGCTGGCTTCATGACCTTCGTCAAGCAGTACGCGCC	1380
Db	64585	TTTGAACAGCAATTCGAGATGCTGCTGGCTTCATGACCTTCGTCAAGCAGTACGCGCC	64644
QY	1381	GAGTTGCTGACCGGGTACAAATCATCAATCTTCGACTGGCCCTTCGCTCTGACCAAGCTG	1440
Db	64645	GAGTTGCTGACCGGGTACAAATCATCAATCTTCGACTGGCCCTTCGCTCTGACCAAGCTG	64704
QY	1441	ACGGAGATCTTACAAGTCCCGCTCGACGGGTACGGGCGCATGAAACGGCGGGGTGTCTTC	1500
Db	64705	ACGGAGATCTTACAAGTCCCGCTCGACGGGTACGGGCGCATGAAACGGCGGGGTGTCTTC	64764
QY	1501	CGCGTGTGGACATTCGGCCAGAGCCACTTTCAGAAAGCGAGCAAGATCAAGGTGAACGGG	1560
Db	64765	CGCGTGTGGACATTCGGCCAGAGCCACTTTCAGAAAGCGAGCAAGATCAAGGTGAACGGG	64824
QY	1561	ATGGTGAACATCGACATGTACGGATCATCACCGACAAGTCAAACTCTCCAGCTTACAAG	1620
Db	64825	ATGGTGAACATCGACATGTACGGATCATCACCGACAAGTCAAACTCTCCAGCTTACAAG	64884
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QY	1681	ATCCCGCGCTACTACGCTTCGGCGCCCGCGACGCGGGGTGATCGGCGAGTATTGTGTG	1740
Db	64945	ATCCCGCGCTACTACGCTTCGGCGCCCGCGACGCGGGGTGATCGGCGAGTATTGTGTG	65004
QY	1741	CAGGACTCGCTGCTGGTTCGGGCGAGCTGTTCTTCAAGTTTCTGCGCACCTGGAGCTTCC	1800
Db	65005	CAGGACTCGCTGCTGGTTCGGGCGAGCTGTTCTTCAAGTTTCTGCGCACCTGGAGCTTCC	65064
QY	1801	GGCGTTCGGCGCTTCGGCGGGCATCAACATCACCGGCACCATCTTACGACGGCCAGCAGATC	1860
Db	65065	GGCGTTCGGCGCTTCGGCGGGCATCAACATCACCGGCACCATCTTACGACGGCCAGCAGATC	65124
QY	1861	CGCGTCTTACGTGCTCTGCGCTTCGGGCGCAGAAAGGCTTCACTCTCGCGGACACC	1920
Db	65125	CGCGTCTTACGTGCTCTGCGCTTCGGGCGCAGAAAGGCTTCACTCTCGCGGACACC	65184

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Db 66325 GAGCCCATCGCGCATACCGACCCCGGAGAGGACATCCAGACTTTGTCTCAAGGCC 66384
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Qy 3415 AAGCTGCTGGTTCGAGCTGGCGGAGGATCCCGGATCGCCATCGCCCGGCGGTCCG 3474
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Qy 3535 CTGTTTGGAAATAACGCCAAGATCAACGAGTCTGTTAAAGAGTTTATTCGCCGAGACG 3594
Db 66805 CTGTTTGGAAATAACGCCAAGATCAACGAGTCTGTTAAAGAGTTTATTCGCCGAGACG 66864
Qy 3595 TGCGACCCCGCGACGAGCTGGCGCGCGCGCTCAGGGCGCGGGTTCCGGCGCGGGGG 3654
Db 66865 TGCGACCCCGCGACGAGCTGGCGCGCGCGCTCAGGGCGCGGGTTCCGGCGCGGGGG 66924
Qy 3655 GCGCGGCTACGCGGAGGAACTCGTCAATGTTGCATAGAGCTTTGATCTCTAGCA 3714
Db 66925 GCGCGGCTACGCGGAGGAACTCGTCAATGTTGCATAGAGCTTTGATCTCTAGCA 66984
Qy 3715 TGA 3717
Db 66985 TGA 66987

RESULT 4

US-09-904-065-5

; Sequence 5, Application US/09904065

; Patent No. 6682892

; GENERAL INFORMATION:

; APPLICANT: Homa, Fred

; APPLICANT: Wathen, Michael

; APPLICANT: Hopkins, Todd

; APPLICANT: Thomsen, Darrell

; TITLE OF INVENTION: A Method for Treating Herpes Virus

; FILE REFERENCE: 00221

; CURRENT APPLICATION NUMBER: US/09/904,065

; CURRENT FILING DATE: 2001-07-12

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5

; LENGTH: 3708

; TYPE: DNA

; ORGANISM: herpes simplex

US-09-904-065-5

Query Match 82.3%; Score 3059.8; DB 4; Length 3708;
Best Local Similarity 89.3%; Pred. No. 0;
Matches 3321; Conservative 0; Mismatches 387; Indels 9; Gaps 2;
Qy 1 ATGTTTGTGTCG 60
Db 1 ATGTTTGTGTCG 60
Qy 61 TCTGGGTTTTTTCG 120
Db 61 TCGGGTTTTTTCG 117
Qy 121 CGCGCGCAGAACTTCTACAAACCCCACTCGCTCAGACCGGAAACGACGCGCGCGCGCG 180
Db 118 TTGAGGCAAACTTTTACAAACCCCACTCGCTCAGACCGGAAACGACGCGCGCGCGCG 177
Qy 181 GGGCGGCTCAGCGCGCATACGTACTACAGCGAGTGCAGCAATTTTCGATTTATGCGCGCG 240
Db 178 GGGCGCAACCGCGCGCATACGTACTATAGCAATGCGATGAAATTTTCGATTTATGCGCGCG 237
Qy 241 CGTTCGCTGAGAGGACCG 300
Db 238 CGGCTGCTGAGAGGATGCG 297
Qy 301 CG 360
Db 298 AAGCG 357
Qy 361 GAGGGCTTCG 420
Db 358 GCGCGCTTCG 417
Qy 421 TTGCGACCCCG 480
Db 418 TTCAACCCCG 477
Qy 481 TACAGCATCG 540
Db 478 TACGCGATCG 537
Qy 541 ACCGTCATCAACCGCTGCGTCTGAGTCTGACCCCGAGGCGCATCGCGTCCCGTTACGCTAC 600
Db 538 ACCGTCATCAACCGCTGCGTCTGAGTCTGACCCCGAGGCGCATCGCGTCCCGTTACGCTAC 597
Qy 601 GGCACG 660
Db 598 GGCACG 657
Qy 661 GCG 720
Db 658 GCG 717
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Db 718 TTTCCGCGCGCATCTCG 777
Qy 781 TATTAGAAACG 840
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Qy 841 GCGTACCTGTGCGCAAACTTTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Db 838 TCGTACCTGTGCGCAAACTTTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 897
Qy 901 ACCACCGGTTTATCTGCGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
Db 898 ACCACCGGTTTATCTGCGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 957
Qy 961 CCGCGCGCGCGGAAACG 1020
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Qy 1021 GACGTCGAGTTTAACTGCGACGCGCGGACAACTTGGCGCGTTCGAGGGGCGCATGTGTGACCTG 1080

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1138 GCCTTTCGGTTCGGGGGACCGCGAGGACCTGGTATTCAGATATCCCTGTCTGTCTAC 1197
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1198 GACCTGTCCACACCGCCCTCGAGACATCCCTCTGTTTTCGCTCGGATCCCTCGACCTTC 1257
1261 CCGGAGTCCCACTCAGCGATCTCGCTCCAGGGGCTCGCGGCCCGCTCGTCTGTGAG 1320
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1438 ACGGACATTTACAAGGTCCCGTTCGACGGGTACGGGCGCATGAACGGCGGGGTGTGTTT 1497
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1618 CTCAACCGCGTTCGGGAGCGCTTCGAGAGGACAAAGAAAGGACCTGAGCTATCGCGAC 1677
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1678 ATCCCGCGCTACTAGCCCGCGGGGCCCGCGAAGCGGGGTGATCGGCGAGTACTGCATA 1737
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1738 CAGGATTCCTGTGTGGCCAGCTGTTTTCAGTTTTCAGTTTTCGCCCATCTGGAGCTCTG 1797
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1858 CCGCTTTCACGTGCTCTCGGCTTCGAGAGGGGCTTCATCTCGCGGACACC 1917
1921 CAGGGGCGGTTTCGGGGCTTCGACAAAGAGGGGCGCCCAAGCGCCGCGCTGTCTCGGGG 1980
1918 CAGGGGCGATTTAGGGGCGCGGGGGGAGGGCGCCCAAGCGTCCGGCGCAGCCCCGGAG 1977
1981 GAAGGGGAGCGCGCGGGGACGGGAAACGGGGACGAGGATAAGGACGACGAGACGAG 2040
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2041 GACGGGACGACGCGAGAGGAGTTCGCGCGAGACCGGGGCGCGACGCTGCGGTACCAAG 2100
2032 GGGGGGACGGGAGCGGGAGGGCGCGGGAGACCGCGCGGACGCTGGGGTACCAAG 2091
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2152 TTTGCGACGCTGTATACCCAGAGCATCATCCAGGCCCAAACTGTGTCTTCAGTACGCTCTCC 2211
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2212 CTGAGGGCGGACGAGTGGCGACCTGAGGGGGCAAGGACTACTCTGGAGATCGAGGTG 2271
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2401 GAGGAGGCGGCTCTCTCTCGACAAGCAACAGCGCGCATCAAGGTGGTGTGCAACTCGGTG 2460
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2872 GTGCGCAAAACAACCTGCGGTTTATCAACCGACCTCCAGGGCCCTGTCGACCTGCTG 2931
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2992 TGGTGGCGCGACCCCTGCGCGAGGAGATGCAAGGGCTTCGAGGGCGCTCTCTGTAAGCGC 3051
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3112 AGCAGACACCGCGCGCTTACCAACAAAGCGCTTGGCCCACTGACCGGTGTATTACAAG 3171
3181 CTCTATGGCGCGCGCGGAGGATCCGCTCCATCAAGGACCGGATCCCGTACGTGATCGTG 3240
3172 CTCTATGGCGCGCGCGGAGGATCCGCTCCATCAAGGACCGGATCCCGTACGTGATCGTG 3231

QY 3241 GCCCAGACCCGCGAGGTAGAGGACGGTCCGCGGCTGGCGCCCTCCCGAGCTAGAC 3300
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QY 3301 GCCCGCCGCCAGGAGGACGCGCCGCCGCCCGCCAGCGCCCTGCGCTCCCGGCGAGCGC 3360
DB 3292 GCCCGCCGCCAGGAGGACGCGCCGCCGCCCGCCAGCGCCCTGCGCTCCCGGCGAGCGC 3351
QY 3361 CCCCGGAGACGCGCTGCATGCGACCCGCCCGGAGGCGCTCCAGCCGCCCAAGCTG 3420
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DB 3412 CTGGTGTCCGAGTGGCGGAGATCCCGGAGTACGCCATCCCGGCGTTCGCGCTCAAC 3471
QY 3481 ACGGACTATTACTTCTCCACCTGCTGGGGGCGGCTGCGTGAAGGCGCTGTTT 3540
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DB 3592 CCCCGGAGACGCTGGCGCGGCTCAGGGCGCGGCGGTTTCGGGCGCGGCGGCGCGC 3651
QY 3661 GCTACGGCGAGAAACTGTCGAATGTTGCATAGAGCCTTGTATCTTAGCATGA 3717
DB 3652 GCTACGGCGAGAAACTGTCGAATGTTGCATAGAGCCTTGTATCTTAGCATGA 3708

RESULT 5

US-08-680-326-29
; Sequence 29, Application US/08680326
; Patent No. 5925733
; GENERAL INFORMATION:
; APPLICANT: ROSE, TIMOTHY M.
; APPLICANT: BOSCH, MARINX
; APPLICANT: STRAND, KURT
; APPLICANT: TODARO, GEORGE J.
; TITLE OF INVENTION: DNA POLYMERASE OF GAMMA HERPES VIRUSES
; TITLE OF INVENTION: ASSOCIATED WITH KAPOSI'S SARCOMA AND RETROPERITONEAL
; TITLE OF INVENTION: FIBROMATOSIS
; NUMBER OF SEQUENCES: 152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/680,326
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 29938-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 3708 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-680-326-29

Query Match 82.1%; Score 3053.4; DB 2; Length 3708;
Best Local Similarity 89.2%; Pred. No. 0;
Matches 3317; Conservative 0; Mismatches 391; Indels 9; Gaps 2;

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DB 61 TCGGGTTTTTTTTCGCGCGCGCGCGCTCGGGAGCCGGCC---GGGAGCCCCCGCTTGC 117
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DB 478 TAGGCGATCGCGCGCCAGTTTCCACGCGCGTTTATGAGCGCCATCAACCGAGCGG 537
QY 541 ACGGTATCAGCGTCTGGGTCTGACCCCGAAGGCGATCGGTCCGCTTACGCTCTAC 600
DB 538 ACCGTATCAGCGTCTGGGCTGATCCGGAAGGCGACCGGGTGGCGCTTACGCTTAC 597
QY 601 GGCAGCGCGCGTACTTTTACATGAACAGGCGGAGGTGATCGGCACCTGCAAGTGCCT 660
DB 598 GGCAGCGCGCGTACTTTTACATGAACAGGAGGAGGTGCAAGGACCTTACATGCCCG 657
QY 661 GCGCGCGCGATCTCTGCGAGCGCTTGGCGCGCGCTTGGCGAGTTCGCGGGGGGCTG 720
DB 658 GCGCGCGAGATCTCTGCGAGCGCATGCGCGCGCTTGGCGAGTTCGCGGGCGGCTG 717
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DB 718 TTCGCGGCGATTTCCGCGGACCATTCGAGGCGGAGGTGCTGAGCGCGCGCGCTGAT 777
QY 781 TATTAGAAACGCGCGCGCTTACTACCGCTTCTGTCGAAGCGGGCGCGCGCTG 840
DB 778 TACTAGAGCGCGCGCTCTGTTTACCGGCTTCTGTTTACCGGCTTCTGGAAGCGCGCGCTG 837
QY 841 GCCTACCTGTGCGACAACTTTTCCCGCGCATCAGGAAGTACGAGGGGGCGCTCGACGCG 900
DB 838 TGTACCTGTGCGACAACTTTCTCCCGCGCATCAAGAAAGTACGAGGTGGGTCGAGCGC 897
QY 901 ACCACCGGTTTTATCTGTGAGCAACCCGGGGTTTGTACCTTCGGCTGGTACCGCTCAAG 960
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Db	958	CCGGCCCGGAACAACACGCTAGCCAGCCGCGGCCCCGATGGCTTCGGGACATCCAGC	1017	Db	2032	GGGGCGAGCGGAGACCGGACCGCGCGCGGAGACCGCGCGCGGACGTTGGGTACCAG	2091
QY	1021	GACGTGAGTTTAACTGACGCGGACACACTGCGCGTTCGAGGGGCGCATGTGTACCTG	1080	QY	2101	GGGGCCCGGGTCTCTCGACCCACCTCCCGGTTTACAGTCGACCCCGTGGTGTGTGTGAC	2160
Db	1018	GACGTGAGTTTAACTGATCGCGGACAACTGGGCCATCGAGGGGGCATGAGCACCTA	1077	Db	2092	GGGGCAGGGTCTTGACCCCACTTCCGGGTTTACGTGAACCCCGTGGTGTGTGTGAC	2151
QY	1081	CCGGCTTACAAGCTCATGTCTTCGATATCGAATCGAAGCCGCGGGGAGAGCAGCTG	1140	QY	2161	TTTTCAGCCTGTATACCCAGCATCATCAGGCCCCAACCTGTGTCTCAGTACGCTCTCC	2220
Db	1078	CCGGCATACAGCTCATGTCTTCGATATCGAATCGAAGCCGCGGGGAGAGCAGCTG	1137	Db	2152	TTTTCAGCCTGTATACCCAGCATCATCAGGCCCCAACCTGTGTCTCAGCAGCTCTCC	2211
QY	1141	GCCTTTCGGTTCGGGAACGCCGGAAGACCTCGTATCCAGATCTCTGTCTGTCTAC	1200	QY	2221	CTGGGCGCGAGGCCGTTCGGCACTGAGAGGGGACCGGGAATCTCTGAGATCAGGTG	2280
Db	1138	GCCTTTCGGTTCGGGCAACCGGAGGACCTGGTCAATCCAGATATCTCTGTCTGTCTAC	1197	Db	2212	CTGAGGGCGAGCGAGTGGCGCACCTGGAGGGCGGCAAGGACTACCTGGAGATCAGGTG	2271
QY	1201	GACCTGTCCACACCGCCTCGAGCACATCTCTGTTTTCGCTCGGATCTCGGACCTC	1260	QY	2281	GGGGCCCGACCGCTCTCTGTAAGGCCCAAGTACGCGAGAGCTGCTGAGCATCTCTG	2340
Db	1198	GACCTGTCCACACCGCCTCGAGCACATCTCTGTTTTCGCTCGGATCTCGGACCTC	1257	Db	2272	GGGGGCGACCGCTGTCTTCTGTAAGGCTCAGTGGAGAGAGCTCTCTCAGCATCTCTC	2331
QY	1261	CCGGAGTCCCACTCAGCGATCTCGCTCCAGGGGCTCGCGGCCCGCTCTCTCTGGAG	1320	QY	2341	CTGCGCATGGCTGGCCATCGAAGCAGATCCGCTCGCGATCCCCAGAGCACCCCC	2400
Db	1258	CCGGAATCCCACTGNAAGCTGGGGCCAGGGCTCGCCACGCCGTGGTCTTGGA	1317	Db	2332	CTGCGGACTGGCTCGCATCGAAGCAGATCCGCTCGCGATTTCCAGAGCACCCCC	2391
QY	1321	TTTGAAGGAAATTCGAGATGCTGTGGCTTCATGACCTTCGTCGTCGTCGTCGTCG	1380	QY	2401	GAGGAGCGCTCTCTCTCGACAAAGCAAGGCGGCATCAAGGTGGTGTGCACTCGGTG	2460
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QY	1381	GAGTTCGTGACCGGTTACAAATCATCAATTCGACTGCGCTCTCTCTGACCAAGCTG	1440	QY	2461	TACGGTTTACCGGGCGCAGCAGCTCTCTGCTGCTGCTGCACTGGCGCCACCGGTG	2520
Db	1378	GAGTTCGTGACCGGTTACAAATCATCAATTCGACTGCGCTCTCTCTGACCAAGCTG	1437	Db	2452	TACGGTTTACCGGGAGTCAGCAGCAGCTCTGCTGCTGCTGCACTGGCGCGAGGTG	2511
QY	1441	ACGGAGATCTACAAGGTCCCGCTCGACGGGTACGGGCGCATGAACGGCGGGTGTTC	1500	QY	2521	ACGACCATCGGCGCGAGATGCTCTCGCAGCGCGGTACGTGCAACGCGCTGGGG	2580
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Db	1858	CGCGTTCACGTGCTCTCGGCTTGGGGCGCAGAGGGCTTCATCTGCGCGACACC	1917	Db	2932	TTTTACGAGTACCTGATTCGGAGCGCGCGGTTAGCGAGCGCGCCCGCAGAGGAG	2991
QY	1921	CAGGGCGGTTTCGGGGCTCGACAAAGAGGGCGCCCAAGCGCCCGGCTGCTCGGGG	1980	QY	3001	TGGCTGGGCGGACCCCTGCGCGAGGAGTCAAGGGCTTCGGGGCCCTCTCTGAGACGCC	3060
Db	1918	CAGGGCGGTTTTCGGGGCTCGACAAAGAGGGCGCCCAAGCGCCCGGCTGCTCGGGG	1977	Db	2992	TGGCTGGGCGGACCCCTGCGCGAGGAGTCAAGGGCTTCGGGGCCCTCTCTGAGACGCC	3051
QY	1981	GAGGGGAGCGCCCGGGGACCGGGAACCGGGGACGAGGATTAAGGATCAAGCAGGACGAG	2040	QY	3061	CATCGCGGATCAACCGACCGGAGAGGAGCATCAAGGACTTGTCTCTACCCCGGACTG	3120
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				QY	3121	AGCAGACACCGCGCGGTACACCAAGCGCCTGGGCCACCTGACGGTGTATTACAAG	3180


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RESULT 6

US-09-904-065-7

; Sequence 7, Application US/09904065

; Patent No. 6682892

; GENERAL INFORMATION:

; APPLICANT: Homa, Fred

; APPLICANT: Mathen, Michael

; APPLICANT: Hopkins, Todd

; APPLICANT: Thomsen, Darrell

; TITLE OF INVENTION: A Method for Treating Herpes Virus

; FILE REFERENCE: 00221

; CURRENT APPLICATION NUMBER: US/09/904,065

; CURRENT FILING DATE: 2001-07-12

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7

; LENGTH: 3708

; TYPE: DNA

; ORGANISM: herpes simplex

US-09-904-065-7

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Query Match      82.1%; Score 3053.4; DB 4; Length 3708;
Best Local Similarity 89.2%; Pred. No. 0;
Matches 3317; Conservative 0; Mismatches 391; Indels 9; Gaps 2;
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RESULT 7

US-09-904-065-9
; Sequence 9, Application US/09904065
; Patent No. 6682892
; GENERAL INFORMATION:
; APPLICANT: Homa, Fred
; APPLICANT: Wathen, Michael
; APPLICANT: Hopkins, Todd
; APPLICANT: Thomsen, Darrell
; TITLE OF INVENTION: A Method for Treating Herpes Virus
; FILE REFERENCE: 00221
; CURRENT APPLICATION NUMBER: US/09/904,065
; CURRENT FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 3708
; TYPE: DNA
; ORGANISM: herpes simplex
US-09-904-065-9

Query Match 82.0%; Score 3047; DB 4; Length 3708;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 3313; Conservative 0; Mismatches 395; Indels 9; Gaps 2;

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DB 178 GGGCCAAACCCAGCGCATAGTACTACAGGAGTGCAGGAGTTCGATTCATTCGCCCCG 237
QY 241 CGTTCTCGAGAGAGAGCCCGCGGAGCGAGCGCACCGGGTTCACGACGCGCCCTC 300
DB 238 CGGGTCTGGACAGAGATGCCCCCGGAGAGCGCGCGGGTGCACGACGCTCACCTC 297
QY 301 CGCGCGCGCCCTAAGGTGTACTCGGGGGGAGCAGCGGAGCGTCTCGCGCTGGGCCCG 360
DB 298 AAGCGCGCCCCAAGGTGTACTCGGGGGGAGCAGCGGAGCGTCTTCGCGCTCGGGTCG 357
QY 361 GAGGGTCTTCGCGCGCTGCTTGGCCCTGTGGGCGGTTCGGAACCATGCCCCCAAGGGG 420
DB 361 GAGGGTCTTCGCGCGCTGCTTGGCCCTGTGGGCGGTTCGGAACCATGCCCCCAAGGGG 420

DB 358 GGCGGCTTCTGGCGCGCGCGCTCGCGCTGTGGGGCGGGTGGACACACGCCCGCGGGG 417
QY 421 TTTCGACCCACCGTCAACCGTCTTCACAGTGTACGACATCTTCGAGCAGCAGTGGAAACGCG 480
DB 418 TTCAACCCACCGTCAACCGTCTTCACAGTGTATGACATCTTCGAGAACCTGGAGCAGCG 477
QY 481 TACAGCATCGCGCGCGCGCGCTTCACAGAGCGATTTATGAGACGCCATTCACGCCCGCGGG 540
DB 478 TAGGGCATCGCGCGCGCGCGCTTCACAGCGCGGTTTATGAGCGCATCACACGCGGG 537
QY 541 ACGTCATCAGCGTCTTCGGGTCTGACCCCGGAAGGCATCGCTCGCGCTTCACGCTTAC 600
DB 538 ACCGTTCATCAGCTCTCGGGCTGACTCGGAAGGCACCGGGTGGCGCTTCACGTTTAC 597
QY 601 GGCAGCGCGAGTACTTTTACATGAACAAGGGGAGGTGATCGGCACTTCGCAAGTGCCT 660
DB 598 GGCAGCGCGAGTACTTTTACATGAACAAGGGGAGGTGATCAGGCACTTCACATGCGCG 657
QY 661 GCCCGCGCGATCTCTCGAGAGCGCTTGGCGGGCGCTTCGCGAGTTCGCGGGGGGTTCG 720
DB 658 GCCCGCAGAGATCTCTCGAGAGCGCATGGCGCGCGCTTCGCGAGTTCGCGGGCGGTTCG 717
QY 721 TTTCGCGGATCTCTCGCGACCACTTCGAGAGCGAGGTGTGGAGCGCGCGAGCTGTAC 780
DB 718 TTTCGCGGATCTCTCGCGACCACTTCGAGAGCGAGGTGTGGAGCGCGACCGAGCTGTAC 777
QY 781 TATTAGGAACGCGCGCGCGCTTACTACCGCTCTTCGTCGAAGCGGGCGCGCGCTG 840
DB 778 TACTAGAGAGCGCGCGCGCTCTGTTTACCGGCTCTAGTTCGAAGCGGGCGCGGTCTG 837
QY 841 GCTTACTCTGCGCAAACTTTTGCCTCCCGGATCAGGAAGTACGAGGGGGCGTTCGACGCC 900
DB 838 TCGTACTCTGCGCAAACTTTTGCCTCCCGGATCAGGAAGTACGAGGGGTTCGAGGCC 897
QY 901 ACCACCGGTTTATCTGAGCAACCGCGGGTTCCTTACCTTCGGCTGGTACCGCCCTCAAG 960
DB 898 ACCACCGGTTTATCTGAGCAACCGCGGGTTCCTTACCTTCGGCTGGTACCGCTTCAA 957
QY 961 CCGGGCGGGGAACGCGCGCGCGCCCAACCGCGCGCCCGCGAGCTTCGGAACCTCGAGC 1020
DB 958 CCGGGCGGGGAACCAACAGCTAGCCAGCGCGGGCGCGCGCTTCGGGACATTCAGC 1017
QY 1021 GAGCTGAGTTTAACTGCGCGGCAACCTTCGGCGTTCGAGGGGGCGTGTGTGACCTG 1080
DB 1018 GATGTCGAGTTTAACTGTACGCGGCAACCTTCGGCGATCAGAGGGGGCATGACGACCTA 1077
QY 1081 CCGGCTTACAGCTCATGTCTTCGATATCGAATGCAAGCGCGGGGGAGGAGGAGCTG 1140
DB 1078 CCGGCATACAGCTCATGTCTTCGATATCGAATGCAAGCGGGGGGGAGGAGGAGCTG 1137
QY 1141 GCCTTTCGGTTCGCGGAACGCGCGGGAAGACCTTCATCCAGATCTCTGTCTGTCTAC 1200
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QY 1321 TTTGACAGGAATTCGAGATGCTGTGGCTTCATGACCTTCGTCAAGCAGTACGCGCCC 1380
DB 1318 TTTGACAGGAATTCGAGATGCTGTGGCTTCATGACCTTCGTCAAGCAGTACGCGCCC 1377
QY 1381 GAGTTCGTGACCGGGTACAACTCATCACTTCGAGTGGCCCTTCGTTCCTGACCAAGCTG 1440
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QY 1441 ACGGAGATCTCAAGGTCCTCGCTCGAGCGGGTACGCGCGCATGAACGCGCGGGGTGTGTT 1500
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Db	1498	CCGCTGTGGGACATAGGGCCAGAGCCACTTCCAGAAAGCGCAGCAAGATAAAGGTGAACGGC	1557	Db	2572	GCCTTCGAACAGCTCCTGGCCGATTTCCGGAGGGCGCGACATCGCGCCCGCCCGGGCCC	2631
QY	1561	ATGGTGAACATCGATGATGAGGATCATCACCAGCAAGGTCAAACTCTCAGCTTACAAG	1620	QY	2641	TACTCCATCGCATCATCTACGGGACACGACTCAATTTTCTGTTTGTGCGCGGCGCTC	2700
Db	1558	ATGGTGAACATCGATGATGAGGATTAACCCGACAAAGATCAAGCTCTCGAGCTACAAG	1617	Db	2632	TATTCATCGCATCATCTACGGGACACGACTCCATATTTGTGCTGTGCGCGGCGCTC	2691
QY	1621	CTGAACCGCGTCCCGAGGCCCTCTTGAAGGACAAGAAAGGATCTGAGCTTACCGCGAC	1680	QY	2701	ACGGCCGGCGCTGGTGGCCATCGGCGACAAAGATGGCGAGCCACATCTCGCGCGCGCTG	2760
Db	1618	CTCAAGCGCGTCCCGAGGCCCTCTGAAGGACAAGAAAGGATCTGAGCTTACCGCGAC	1677	Db	2692	ACGGCCGGCGCTGACGGCCGTGGCGACAAGATGGCGAGCCACATCTCGCGCGCGCTG	2751
QY	1681	ATCCCGCGCTACTACGCTCTCGGCGCCGCGCAGCGGGGTGATCGGCGAGTATTTGTG	1740	QY	2761	TTCTCTCCCGCATCAAGCTCGAGTGCAGAAAAAGTTTCAACAAGCTGCTGCTCATCGCC	2820
Db	1678	ATCCCGCACCTACTACGCGCGCGCGCGCCGCGCAACGCGGGGTGATGGCGAGTACTGCATA	1737	Db	2752	TTTCTGCGCCCGCATCAAACTCGAGTGCAGAAAGAGTTTCAACAAGCTGCTGCTGATCGCC	2811
QY	1741	CAGGACTCGCTGCTGGTGGGCGAGCTGTCTTCAAGTTTCTGCGCAGCTCGAGCTTTCC	1800	QY	2821	AAGAAAAAGTACATCGGCGTCACTCGCGGGGCAAGATGCTCATCAAGGGCGTGGATCTG	2880
Db	1738	CAGGATTCCTGCTGGTGGGCGAGCTGTCTTAAAGTTTTCGCCCATCTGGAGCTCTCG	1797	Db	2812	AAGAAAAAGTACATCGGCGTCACTACCGGGGTAGATGCTCATCAAGGGCGTGGATCTG	2871
QY	1801	GCGGTGCGCGCTCGCGGGCATCAACATACCCGCAACCATCTACGACGGCCAGCAGATC	1860	QY	2881	GTGCGCAAAAAAACTGCGCGTTTATCAACCGCACCTCOAGGGCCTTGGTCGACTGCTG	2940
Db	1798	GCCGTGCGCGCTTGGCGGGTATTAACTACCCGCAACCATCTACGACGGCCAGCAGATC	1857	Db	2872	GTGCGCAAAAAAACTGCGCGTTTATCAACCGCACCTCOAGGGCCTTGGTCGACTGCTG	2931
QY	1861	CGCGTCTTACGCTGCTCTGCGCTTGGCGGCCAGAGGGCTTCACTCTGCGGACACC	1920	QY	2941	TTTTACGACGATACGTTATCCGAGCGCGCGCGGTTAGCGAGGCGCCCGCAGAGGAG	3000
Db	1858	CGCGTCTTACGCTGCTCTGCGCTTGGCGGCCAGAGGGCTTATTTCTGCGGACACC	1917	Db	2932	TTTTACGACGATACGTTATCCGAGCGCGCGCGGTTAGCGAGGCGCCCGCAGAGGAG	2991
QY	1921	CAGGGCGGTTTCGGGGCTCTCACAGGAGGCGCCCAAGCGCCCGCGCTGCTCGGGGG	1980	QY	3001	TGGCTGGCGCACCCCTGCCGAGGGACTGACAGGGCTTTCGGGGCGCTCTCGTAGACGCC	3060
Db	1918	CAGGGCGGATTTAGGGGCGCCCGGGGGAGGGCGCCCAAGCTCCGGCGCGACCCCGGGAG	1977	Db	2992	TGGCTGGCGCACCCCTGCCGAGGGACTGACAGGGCTTTCGGGGCGCTCTCGTAGACGCC	3051
QY	1981	GAAAGGGAGCGCCCGGGGACCGGGAACCGGGGACGAGGATTAAGGACGACGACGAGGACGAG	2040	QY	3061	CATCGCGCATCACCGACCCGAGAGGGAATCCAGGACTTTTGTCTCAACCGCCGAACTG	3120
Db	1978	GACGAGGAGCGCCAGAGGAGGGGAGGAGC-----AGAACGACGCGAGGAGGC	2031	Db	3052	CATCGCGCATCACCGACCCGAGAGGGAATCCAGGACTTTTGTCTCAACCGCCGAACTG	3111
QY	2041	GACGGGACGACGGGAGAGGTGCGCGCGAGACCGGGGGCGGAGCTTGGGTACCG	2100	QY	3121	AGCAGACCCCGCGCGGTACACCAACGAGCGCTGCGCCCACTCACCGTGTATTACAAG	3180
Db	2032	GGGGGCGACGGGAGCGGAGGGCGCGGGAGACCGCGGCGGCACTGTTGGGGTACCAG	2091	Db	3112	AGCAGACCCCGCGCGGTACACCAACGAGCGCTTGGCCCACTCACCGTGTATTACAAG	3171
QY	2101	GGGGCCCGGCTCCTGACCCCACTTCGGGTTTACGTCGACCCCGTGTGTGTGAC	2160	QY	3181	CTCATGGCCCGCGCGCAGGTCCGTTCCATCAAGAGACCGGATCCCGTACGTGATCGTG	3240
Db	2092	GGGGCAGGGTCTTTGACCCCACTTCCGGGTTTACGTTGAAACCCCGTGTGTGTGAC	2151	Db	3172	CTCATGGCCCGCGCGCAGGTCCGTTCCATCAAGAGACCGGATCCCGTACGTGATCGTG	3231
QY	2161	TTTTCGAGCTGTACCCAGCATCATCCAGGCCCAACCTGTGTCTCAGTACGCTCTCC	2220	QY	3241	GCCAGACCCCGGAGGTAGAGAGACGCTGCGCGGCTGCGCGCCCTCGCGAGCTAGAC	3300
Db	2152	TTTTCGAGCTGTACCCAGCATCATCCAGGCCCAACCTGTGTCTCAGTACGCTCTCC	2211	Db	3232	GCCAGACCCCGGAGGTAGAGAGACGCTGCGCGGCTGCGCGCCCTCGCGAGCTAGAC	3291
QY	2221	CTGCGGCGGAGCGCTGCGCACCTGAGGGCGACCGGGATACCTGGAGATCGAGTG	2280	QY	3301	GCGCGCGCCAGGGGAGAGCGCCGCCCCCGAGCGGCCCTCGCCCTCCCGGCCAAGCGC	3360
Db	2212	CTGAGGGCGGACGATGCGCACCTTGAAGGCCACGTCACGAGAGCGCTGTGAGCATCTTG	2271	Db	3292	GCGCGCGCCAGGGGAGAGCGCCGCCCCCGAGCGGCCCTCGCCCTCCCGGCCAAGCGC	3351
QY	2281	GGGGCGGACGCGCTGTTCTGTGAAGGCCACGTCACGAGAGCGCTGTGAGCATCTTG	2340	QY	3361	CCCCGGGAGAGCGCTCGCATGCCACCCCGCGGAGGCGGTCCAAGCCCGCGAAGCTG	3420
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QY	2341	CTGCGGCACTGTGCGCATGCGCAAGAGATCCGCTCGCGGATCCCGCAGAGCACCCCC	2400	QY	3421	CTGTGTCCGAGCTGGCGGAGATCCCGGGTACGCGCATCGCCCGGGGGGTTCGCTCAAC	3480
Db	2332	CTGCGGCACTGTGCGCATGCGCAAGAGATCCGCTCGCGGATCCCGCAGAGCGCCCC	2391	Db	3412	CTGTGTCCGAGCTGGCGGAGATCCCGCATACGCGCATTTGGCCACGCGGTCCGCTGAAC	3471
QY	2401	GAGGAGCGCTCTCTCTGACAGCAACAGGGCGGCATCAAGTGGTGTGCAACTCGTG	2460	QY	3481	ACGGAATATTACTTCTCGACCTGTGGGGCGGCTGCTGACGCTTCAAGGCCCTGTTT	3540
Db	2392	GAGGAGCGCTCTCTCTGACAGCAACAGGGCGGCATCAAGTGGTGTGCAACTCGTG	2451	Db	3472	ACGGAATATTACTTCTCGACCTGTGGGGCGGCTGCTGACGCTTCAAGGCCCTGTTT	3531
QY	2461	TACGGTTTCAAGGGCGGAGACGCTCTTCTGCGCTGCTGCACTGTCGCCCGCCACCGTG	2520	QY	3541	GGAAATAACGCAAGATCAACGAGAGTCTGTTTAAAGAGTGTATTCCCGAGAGCTGGCAC	3600
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QY	2521	ACGACCATCGCGCGAGATGCTCTCGCAACCGCGCGGTACGTGCAACGCGCGCTGGCG	2580	QY	3601	CCCCCGGAGAGCTGGCGCGGCTCAGGGCCCGGGGTTCCGGCCCGCGGGCGCGC	3660
Db	2512	ACGACCATCGCGCGAGATGCTCTCGCAACCGCGCGGTACGTGCAACGCGCGCTGGCG	2571	Db	3592	CCCCCGGAGAGCTGGCGCGGCTCAGGGCCCGGGGTTCCGGCCCGCGGGCGCGC	3651
				QY	3661	GCTACGGCGGAGAAACTCGTCGAATGTTGCATAGAGCCTTTGATACTCTAGCATGA	3717

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Db 3652 GCTACGCGGAGGAAATCGTCGAAATGTCATAGACCTTTGATACCTAGCATGA 3708
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RESULT 8
5223391-4
; Patent No. 5223391
; APPLICANT: COEN, DONALD M.; DIGARD, PAUL E.
; TITLE OF INVENTION: INHIBITORS OF HERPES SIMPLEX VIRUS
; REPLICATION
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/482,634
; FILING DATE: 21-FEB-1990
; SEQ ID NO:4:
; LENGTH: 1654
5223391-4

Query Match 30.0%; Score 1116.6; DB 6; Length 1654;
Best Local Similarity 82.6%; Pred. No. 1.6e-207;
Matches 1373; Conservative 0; Mismatches 184; Indels 106; Gaps 4;

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QY 1470 GTACGGCGCATGAACGGCCGGGGTGTGTTCCGCGTGTGGGACATCGGCCAGAGCCACTT 1529
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RESULT 9
5223391-4
; Patent No. 5223391
; APPLICANT: COEN, DONALD M.; DIGARD, PAUL E.
; TITLE OF INVENTION: INHIBITORS OF HERPES SIMPLEX VIRUS
; REPLICATION
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/482,634
; FILING DATE: 21-FEB-1990
; SEQ ID NO:4:
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i 5223391-4
LENGTH: 1654
Query Match 30.0%; Score 1116.6; DB 6; Length 1654;
Best Local Similarity 82.6%; Pred. No. 1.6e-207;
Matches 1373; Conservative 0; Mismatches 184; Indels 106; Gaps 4;
QY 1351 TTCATGACCTTCGTGACAGATACGGCCCCCGAGTTCTGTCACCGGTACACATCATCAAC 1410
D 1 TTTATGACCTTCGTGAAACAGTACGGCCCCCGAGTTCTGTCACCGGTACACATCATCAAC 60
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1252 GACGCTGTACGACCATCGGCGCGGAGATGCTCTCTCGGACCGCGGAGTACGTCCAGCGG 1311
2574 CTGGCGGAGTTCGATCAGCTGCTGGCGGACTTTTCCGGAGGCGCGGATCGCGGCGCC 2633
1312 CTGGCGGCGCTTCGAAAGCTCTCTGGCGGATTTCCCGAGGCGCGGACATCGCGCGC 1371
2634 CGGTCGCTATCTCATGCGGATCATCTACGGGACAGGACTCCATTTTCTGTTTGTGCGG 2693
1372 CGGGCGCTATTTCATGCGCATCATCTACGGGAGACCGGACTCCATTTTGTGCTGCGG 1431
2694 CGGCTCTACGCGCGCGGCGCTGCTGGCCATGCGGACAAAGATGGGAGCCACATCTCGG 2753
1432 CGGCTCTACGCGCGCGGCGTGAACCCATGCGGACAAAGATGGGAGCCACATCTCGG 1491
2754 CGCGTGTCTCTCCCGCGATCAAGCTCGAGTGTGAAAGAGGTTTCAACAGCTCTGCT 2813
1492 CGCGTGTCTCTCGCGCGCGGCGCTGCTGGCCATCAAACTCGAGTGTGAAAGAGGTTTCA 1551
2814 CATCCGCAAGAAAGTACATCGGCTCATCTGCGGGGCAAGATGCTCATCAAGGGCT 2873
1552 GATCCCAAGAAAGTACATCGGCTCATCTACGGGGTAAAGTGTCTATCAACCGGCT 1611
2874 GSATCTGTGCGCAAAACAACTGCGCTTTTATCAACCGCAC 2916
1612 GSATCTGTGCGCAAAACAACTGCGCTTTTATCAACCGCAC 1654
RESULT 10
5223391-1
; Patent No. 5223391
; APPLICANT: COEN, DONALD M.; DIGARD, PAUL E.
; TITLE OF INVENTION: INHIBITORS OF HERPES SIMPLEX VIRUS
; REPLICATION
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/482,634
; FILING DATE: 21-FEB-1990
; SEQ ID NO: 1:
; LENGTH: 1678
5223391-1
Query Match 27.1%; Score 1005.8; DB 6; Length 1678;
Best Local Similarity 85.1%; Pred. No. 5.2e-186;
Matches 1148; Conservative 0; Mismatches 197; Indels 4; Gaps 2;
QY 3 GTTTCGTGCGCGGCGGCGCGGCTTCCCGCGGGGAGGTCGGGCGGTTCGGGCGGCTGC 62
D 333 GATGTTTTTCGCTGCGGCGCGCTGCTCCCGGAGGAAAGTTCGGCGGCGGCGGCTC 392
QY 63 TGGGTTTTTTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 122
D 393 CGGGTTTTTTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 449
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QY 123 CCGCGAGAACTTCTAACAACCCCACTCGCTCAGACCGGAACGAGCAAAAGCGCCCGG 182
DB 450 GAGGCAAACTTTTACAAACCTTACCTCGCCAGTCGGGACGCAACAGAAAGCGGACCG 509
QY 183 GCGGGCTCAGGCGCATAGTACTACAGCGAGTGGGAGAAATTTGATTTATCGCCCGCG 242
DB 510 GCCAACCCAGCGCATACGTACTATAGCAATGCGATGAAATTTGATTTATCATCGCCCGG 569
QY 243 TTGCTGGAGAGAGACCGCCCGCGAGACGCGCAACCGGGGTTCACAGCGCGCGCTCCG 302
DB 570 GGTGCTGGAGAGATGATCGCCCGGAGAGCGCGCGGGTGCAGACGCTCACCTCAA 629
QY 303 GCGGCGCCCTAAGTGTACTTGGGGGGGAGAGAGCGCAGCTCTCGCGTGGGCGCGGA 362
DB 630 GCGCGCCCTCAAGTGTACTTGGGGGGGAGAGAGCGCAGCTCTCGCGTGGGTCGGG 689
QY 363 GGGCTTCTGCGCGGTGCTTGGCTTGGCTTGGGGGGTGGGACGATGCCCGCCAAAGGGTT 422
DB 690 CGGCTTCTGCGCGGGCTCGCGCTTGTGGGGCGCGGTGGACACGCGCCCGCGGGGT 749
QY 423 CGACCCCAACCGTCAACCGTCTTCAACGTGTACGACATCTCGAGCAGCTGCGGCAACACGCGTA 482
DB 750 CACCCCAACCGTCAACCGTCTTCAACGTGTACGACATCTCGAGAACGTGGAGCACGCGTA 809
QY 483 CAGCATGCGCGCGCCAGCTCCACGAGCGCAACCGGGGTTCACAGCGCGCGCTCCGCGGAC 542
DB 810 CGGCATGCGCGCGCCAGTTCCAGCGCGCGTTTATGGACGCCATCACACCGAGCGGGAC 869
QY 543 CGTCATCACGCTTCTGGGTCTGACCCCGAAGGCCATCGCGTCCGCGCTTTCACGCTACCG 602
DB 870 CGTCATCACGCTTCTGGGCTGACTCCCGAAGGCCACCGGTGGCGCTTTCACGTTACCG 929
QY 603 CACGCGGACGACTTTTACATGAACAAAGCGAGGTGGATCGCACCTCGAGTGCCTGTC 662
DB 930 CACGCGGACGACTTTTACATGAACAAAGCGAGGTGGATCGCACCTCAATATCGCGCGC 989
QY 663 CCGCGCGAGTCTCTGGAGCGCTTGGCGCGCGCTTGGCGAGTTCGCGGGGCGTCTGTT 722
DB 990 CCCACGAGATCTCTCGAGCGCATGCGCGCGCGCTTGGCGAGTTCGCGGGCGCTGTT 1049
QY 723 CCGGGCATCTCGCGGACCACTTCGAGGCGGAGGTGGTGGAGCGCGCGCGCTGTACTA 782
DB 1050 CCGCGGATCTCGCGGACCACTTCGAGGCGGAGGTGGTGGAGCGCACCGACGTACTA 1109
QY 783 TTACGAAACCGCGCCGACCTGTACTACCGCTTCTCGTGAAGCGGGCGCGCTGCG 842
DB 1110 CTACGAGACGCGCCCGCTCTGTTTACCGCTCTACGTCGGAAGCGGGCGCGTCTGTC 1169
QY 843 CTACCTGTGCGACAACCTTTTGGCCCGCGATCAGGAAGTACAGGGGGGGGTGCGACGCCAC 902
DB 1170 GTACCTGTGCGACAACCTTCTCGCCCGGCATCAAGAAGTACAGGGGTGGGTGCGACGCCAC 1229
QY 903 CACCGGTTTATCTGGAACAACCGGGGTTTGTACCTTCGGTGGTACCGCTCAAGCC 962
DB 1230 CACCGGTTTATCTGGAACAACCGGGTTCGTACCTTCGGTGGTACCGCTCAAAAC 1289
QY 963 CCGCGCGGGAACGCGCGCGCCCAACCGCGCCCGGACGCGGTTCGGAACCTTCGAGCGGA 1022
DB 1290 GGGCGGGAACACACGCTAGGCGAGCGCGCGCGCGCGCGATGGCTTCGGGACATCCAGCGGA 1349
QY 1023 CGTCGAGTTTAACTGACGCGCGGACAACTTGGCGCTGCGAGGGGGCCATGTGTACCTGCC 1082
DB 1350 CGTGGAGTTTAACTGTACGCGCGGACAACTTGGCCATCGAGGGGGGCGATCAGCGACCTACC 1409
QY 1083 GGGCTACAGCTCATGTGCTTTCATATCGAATCGAAGCGCGCGGGGGAGGACGAGTGGC 1142
DB 1410 GGCATACAGCTCATGTGCTTTCATATCGAATCGAAGCGCGGGGGGGCGGACGAGTGGC 1469
QY 1143 CTTTTCGG-GTFCGGGAACGCCCGGAAGACCTCGTCATCCAGATCTCTGTCTCTCTACG 1201
DB 1470 CTTTTCGGGTGGCGGGGACCCGGAGACCTGGTATTGACATATCTGTCTCTCTACG 1529
QY 1202 ACCTGTCCACACCGCCCTCGAGCACATCTCTCTGTTTTCGCTCGGATCCTGCGACCTCC 1261
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DB 1530 ACCTGTCCACACCGCCCTGGAGCAGTCTCTCTGTTTTCGTCGGTTCCTGCGACCTCC 1589
QY 1262 CCGAGTCCACACTCAGGATCTCGCTCCAGGGGCTGCGGGCCCGCTGCTCTGGAGT 1321
DB 1590 CCGAATCCGACCTGAACGAGCTGGCGGCCAGGGGCTGCCACGCGCGTGTCTGGAAT 1649
QY 1322 TTGACAGCGAAATTCGAGATGCTCTCGGCC 1350
DB 1650 TCGACAGCGAATTCGAGATGCTGTGGCC 1678

RESULT 11
5223391-1
; Patent No. 5223391
; APPLICANT: COEN, DONALD M.; DIGARD, PAUL E.
; TITLE OF INVENTION: INHIBITORS OF HERPES SIMPLEX VIRUS
; REPLICATION
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/482,634
; FILING DATE: 21-FEB-1990
; SEQ ID NO:1:
; LENGTH: 1678
5223391-1

Query Match 27.1%; Score 1005.8; DB 6; Length 1678;
Best Local Similarity 85.1%; Pred. No. 5.2e-186;
Matches 1148; Conservative 0; Mismatches 197; Indels 4; Gaps 2;

QY 3 GTTTTGTGCGGGCGGGCCGACTTCCCGCGGGGGGAAAGTTCGGCGGCTCGGGCGGCTC 62
DB 333 GATGTTTTCGGTGGCGCGCGCTGTCCCGCGGAGAAAGTTCGGCGGCGAGCGGGCTC 392
QY 63 TGGGTTTTTGGCCCCCAACACCCCGGGGAGCACCCAGACGCGGACCGCGCGCTTCGCG 122
DB 393 CGGGTTTTTGGCGCGCGCGCGCTCGCGAGCGCGCC---GGGGACCCCGCGCTTGT 449
QY 123 CCGGCGAAGACTTCTACAAACCCACCTCGCTCAGACCGGAACGACGCAAGGCCCGCGG 182
DB 450 GAGGCAAACTTTTACACCCCTTACCTCGCCCACTCGGGACGCAACAGAACGCGACCGG 509
QY 183 GCGCGCTCAGCGCCATACGTACTACAGCGAGTGCAGAAATTTTCGATTTATCGCCCGCG 242
DB 510 GCCAACCCAGCGCCATACGTACTATAGCAATGCGATGAATTTTCGATTCATCGCCCGCG 569
QY 243 TTGCTGGAGAGAGACCGCCCGCGGAGCAGCGCACCGGGGTCCACGACGCGCGCTCCG 302
DB 570 GGTGCTGGAGAGCATGCGCCCGCGGAGGAGCGCGCGGGGTGACGACGCTCACCTCAA 629
QY 303 GCGCGCCCTAAGTGTACTTGGGGGGGACGAGCGCGACGCTCTCGGGTGGCGCGGGA 362
DB 630 GCGCGCCCAAGAGTGTACTTGGGGGGGACGAGCGCGACGCTCTCGGGTGGGTGGG 689
QY 363 GGGCTTCTGCGCGGTGCTTGGCTTGGCTTGGGGGGTGGGACCATGCCCGCCAAAGGGTT 422
DB 690 CGGCTTCTGCGCGGGCTCGCGCTTGTGGGGCGCGGTGGACCAACGCGCGGGGT 749
QY 423 CGACCCCAACCGTCAACCGTCTTCAACGTGTACGACATCTCGAGCAACGCGGTA 482
DB 750 CAAACCCCAACCGTCAACCGTCTTTCACGTGTACGACATCTCGAGAACGTGGAGCACGCGTA 809
QY 483 CAGCATGCGCGCGCCAGCTCCACGAGCGAATTTATGGAGCGCCATCACGCCCGCGGGAC 542
DB 810 CGGCATGCGCGCGGCCAGTTCACGCGCGGTTTATGGAGCGCCATCACACCGAGCGGGAC 869
QY 543 CGTCATCACGCTTCTGGGTCTGACCCCGAAGGCCATCGCGTCCGCGCTTTCACGCTACCG 602
DB 870 CGTCATCACGCTTCTGGGCTGACTCCCGAAGGCCACCGGTGGCGCTTTCACGTTACCG 929
QY 603 CACGCGGACGACTTTTACATGAACAAAGCGAGGTGGATTCGGCACTCTGTCTCTCTACG 662
DB 930 CACGCGGACGACTTTTACATGAACAAAGGAGGTGGATTCGAGGAGCTTCAATATGCGCGC 989
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2977 TTAGCCGAGGCGCCCGCAGAGGAGTGGCTGCGCGACCCCTGCCCCGAGGACTGCGAGCG 3036
61 TTAGCCGAGGCGCCCGCAGAGGAGTGGCTGCGCGACCCCTGCCCCGAGGACTGCGAGCG 120
3037 TTGGGGCGGCTCTCTGTAGAGCGCCATCGGGGATACACGACCGCGGAGAGGATCCAG 3096
121 TTGGGGCGGCTCTCTGTAGAGCGCCATCGGGGATACACGACCGCGGAGAGGATCCAG 180
3097 GACTTTGCTCTACCGCGGAACCTAGCAGACACCGCGCGGTACACCAACAGCGCTG 3156
181 GACTTTGCTCTACCGCGGAACCTAGCAGACACCGCGCGGTACACCAACAGCGCTG 240
3157 GCCACCTGACGGTGATTAAAGCTCATGGCCCGCGCGAGGTCCCGTCCATCAAG 3216
241 GCCACCTGACGGTGATTAAAGCTCATGGCCCGCGCGAGGTCCCGTCCATCAAG 300
3217 GACCGGATCCGTACGTGATCGTGGCCGACACCGCGGAGTAGAGGACGGTGGCGCG 3276
301 GACCGGATCCGTACGTGATCGTGGCCGACACCGCGGAGTAGAGGACGGTGGCGCG 360
3277 CTGGCGGCTCTCGCGAGCTAGACGCGCGCGCCCGAGGAGACGCGCCCGCCAGCG 3336
361 CTGGCGGCTCTCGCGAGCTAGACGCGCGCGCCCGAGGAGACGCGCCCGCCCGCG 420
3337 GCCTTGCTCTCCCGGCGCAAGCGCCCGCGGAGACGCGCTGCGATGCGGACCCCGCGGA 3396
421 GCCTTGCTCTCCCGGCGCAAGCGCCCGCGGAGACGCGCTGCGATGCGGACCCCGGGA 480
3397 GCGCGTCAAGCCCGCAAGCTGCTGGTGTGCGAGTGGCGGAGATCCCGGATCCG 3456
481 GCGCGTCAAGCCCGCAAGCTGCTGGTGTGCGAGTGGCGGAGATCCCGGATCCG 539
3457 ATCGCGCGGCGCTTCGCTCAACAGGACTATTCTTCTGACACTGCTGGGGGCGGC 3516
540 ATTGCGGCGGCTGCGCTCAACAGGACTATTCTTCTGACACTGCTGGGGGCGGC 599
3517 TGCGTGACGCTTCAAGGCGCTTGGTAAATGAAAGTACCGAGAGTCTGTTAAAG 3576
600 TGCGTGACATTCAGGCGCTTGGTAAATGAAAGTACCGAGAGTCTGTTAAAG 659
3577 AGTTTATTCGAGAGTGGACACCGCGGAGACGCTGCGCGCGGCTCAGGGCGCG 3636
660 AGTTTATTCGAGAGTGGACACCGCGGAGAGTGGCGCGCGCTCAGGGCGCG 719
3637 GGGTTCGGGCGGCGGCGCGGCTACGGCGGAGAACTGTCGAATGTCATAGA 3696
720 GGGTTCGGGCGGCGGCGGCTACGGCGGAGAACTGTCGAATGTCATAGA 776
3697 GCCTTTGATCTAGCATGA 3717
777 GCCTTTGATCTAGCATGA 797

RESULT 14
US-08-680-326-28
; Sequence 28, Application US/08680326
; Patent No. 5925733
; GENERAL INFORMATION:
; APPLICANT: ROSE, TIMOTHY M.
; APPLICANT: BOSCH, MARINX
; APPLICANT: STRAND, KURT
; APPLICANT: TODARO, GEORGE J.
; TITLE OF INVENTION: DNA POLYMERASE OF GAMMA HERPES VIRUSES
; TITLE OF INVENTION: ASSOCIATED WITH KAPOSI'S SARCOMA AND RETROPERITONEAL
; TITLE OF INVENTION: FIBROMATOSIS
; NUMBER OF SEQUENCES: 152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA

ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,326
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 29938-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 3585 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-680-326-28

Query Match 18.9%; Score 701.8; DB 2; Length 3585;
Best Local Similarity 53.7%; Pred. No. 5.7e-127;
Matches 1659; Conservative 0; Mismatches 1312; Indels 120; Gaps 5;

QY 223 TTTGCAATTTATCGCCCGCGTCTGCTGGAGAGAGCGCCCGCGAGAGCGCGAC 282
DB 127 TTTCAATTTTGGCCCTTAATGTTTAGATGAAGATGTGCCCATGAAGAACAAAGGGG 186
QY 283 GTCCACGACGCGCGCTCCGCGCGCTCTAAAGTGTACTGCGGGGGGACGAGCGCGAC 342
DB 187 GTTCACGTGCGTACACTTAGTCGACGCGCTAAAGTTTACTGTAATGGAAGAAAGTTCCG 246
QY 343 GTCTCTCGGCTGGGCGCGAGGGCTTCTGCGCGCTGCTGGCGCTGTGGCGCGGTGCG 402
DB 247 ATTCTGGATTTTCTGTTTCTCCAGCGCTAGACGCGTGAATTTTGGGGGGAATC 306
QY 403 GACCATGCCCCCAAGGGTTTCACCCCGTCCACCGTCTTCCACGTGTACGACATCCCTG 462
DB 307 GACTTTCGTGGGGAATGTTTACCCCGCTTAAACATTTCCATGATATGATATGTC 366
QY 463 GAGCACGTGGAACACGCGTACAGCATGCGCGCGCGCGCTCCACGAGCGATTTATGGAC 522
DB 367 GAAACAAACAGACCGCGTCTAATGGAGATGTATCC-----CGTTTTCGCACT 414
QY 523 GGCATCACGCGCGCGGACCGTCTACGCTTCTGGGTCTGACCCCGAAGCCATCGC 582
DB 415 GCAACACGACCGCTTGGTACCGCTTATTTACTTGGCATGTCCCGATGTGGAAGAG 474
QY 583 GTGCGGCTTACGCTCTACGCGACGCGGAGTACTTTTACATGAAACAGCGAGGTGGAT 642
DB 475 GTGGGATTCATGTATACGCGATCTGTAATTTTATATATATATATATATATATATATAT 534
QY 643 CGGCACCTGCGAGTGGCGCGCGCGATCTCTGCGAGCGCTTGGCGCG-----693
DB 535 ACCGCTTGTGGCATACGTTCCGCTAGCGAGTTATCTGTATTACTTGGCCGAGTGTTCACG 594
QY 694 -----GCCCTGGCGGAGTGCCTGGCGG 714
DB 595 AGTTCTATGATAACAAATGATGCAACGTTAAATGGAGACAAGAACGCTTTTCATGTT 654
QY 715 GGTGCTTCCCGCGCATCTCCGCGACCATCTTCGAGGCGGAGTGTGTGAGCGCGCGAC 774
DB 655 ACTCGTTTAAAGCGCATCTCCAGAAAGCTTTCGCGTTGAGGTATTGAGCGCACAGAT 714
QY 775 GTGTACTATTACGAAACGCGCGCGCTGTACTACCGCGTCTTCTGTGCGAAGCGCGCGC 834
DB 715 GTTTATTACTAGATACACAGCCATGTGCGTTTACAGGTGTATTCTCCCTCATCTAA 774

QY	835	GGCTGGCCTACCTGTGGACAACTTTTGCCTCCGGATCAGGAAGTACGAGGGGGCGTC	894	QY	1915	GACACCCAGGGCGGTTTCGGGGCTTCGACAAAGGAGCGCCCAAGCGCCCGCGCTGCGCT	1974
Db	775	TTTACAAATATCTTTGTGATAACTTTTCACTCCGGAGTTGAAGATATGAAGTACGGGTA	834	Db	1855	GATGGGGATACCCAGCTACTTTTGAATATAAGGATGTTATTC	1898
QY	895	GAGCGCACACCGCGGTTTATCTTGACAAACCGGGGTTTGTCACTTCGGCTGGTACCGC	954	QY	1975	CGGGGGAAAGGGGAGCGGCGGGGAACGGGGACGAGGATAAGACGACGACGAG	2034
Db	835	GAGCTACCACTCGTTTCTAATGATATCCGGCTTTGTAGTTTGGTTGGTATCA	894	Db	1899	-----CGATGTCGGGATGTTGAGGAA	1920
QY	955	CTCAAGCCCGCGCGGGAAACGGCGGGCCAAACCGCGCCCCCGGACGGCGTTTCGGAAAC	1014	QY	2035	GACGAGACGGGACGAGCGGAGGAGTTCGGCGGAGACCGGGGGCGGCACCTTGGG	2094
Db	895	CTAAAACCTGGAGTTGATGGGAAACGTGTTCGAGTTTCGACCGGCAAGTCGCCAATAAGC	954	Db	1921	GAGATGGATGAAGACGAGAGCGTTTTCCTCCACTGGTACGTCAAGTGGGCGAAATGAGA	1980
QY	1015	TCGAGGAGCTCGAGTTTAACTGACGCGGACACCTTGGCGCTCGAGGGGCGATGTGT	1074	QY	2095	TACGAGGGCGCGGCTCTCGACCCACCTCCGGGTTTACGTTCGACCCCGCTGTGTGTG	2154
Db	955	TTAAGCGAGTTGAAATGACTGCAATGTCGGATAATCTGCAAGCTATACCAACGATGAC	1014	Db	1981	TATAAGAGACGAGGTTTGTGACCTCATACGGGATTTATATCGATCCGGTGTGTA	2040
QY	1075	GACCTGCCGCCCTACAAGCTCATGTCTTCGATATCGAATGCAAGCGCGGGGGAGGAC	1134	QY	2155	TTTGACTTTTGCAGCTGTACCCAGCATCATCAGGCCCAACACTGTGTCTTCAGTACG	2214
Db	1015	TCATGGCTGACTACAAGTTGTATGTTCGATATGATGTAAATCAGGAGATCTAAT	1074	Db	2041	TTGGATTTTCAAGTTTATATCCAAGTATAATTCAGGCCCATTAATTATTTTACCACG	2100
QY	1135	GAGCTGGCCTTTCGGTCCGGAACCGCGGAGACCTCGTCTCATCCAGATCTCTGTCTG	1194	QY	2215	CTCTCCCTGGCGCGGAGCGCTCGCGCACCTGGAGGCGGACCGGACTACCTGGAGATC	2274
Db	1075	GAGCTGGCGTTTCCGATCAACATCTGGAGGATCTGTAAATCCAAATTTCTGTCTA	1134	Db	2101	CTAACGTTTAAATTTTGAACGTTTAAACGTTTGAATCCATCC--GATTATGCCACCTTT	2157
QY	1195	CTCTAGGACCTGTCCACACCGCCCTCGAGCATCTCTCTGTTTTCGTTCGGATCCTGC	1254	QY	2275	GAGGTGGGGGCGGACGCTGTTCTTCGTGAAGGCCACGTACGACGAGAGCTGTCTGAGC	2334
Db	1135	TTATATTCAATCCCTCGACAGTCTTTAGAACACATTTTACTGTTTCCCTTGGCTTTGT	1194	Db	2158	ACAGTTGAGGAAACGTCCTTTTGTGGCTCTAACGTTTCGNAAGTCTGCTGGGT	2217
QY	1255	GACCTCCCGAGTCCACCTCAGCGATCTCGCTCCAGGGGCTCGCGGCCCGCTCGTC	1314	QY	2335	ATCTGTCTGCGCACTGGCTGGCCATCGAAGCAGATCCGCTCGCGATCCCCCAGAGC	2394
Db	1195	GACTTACCAAAAGGTATGTAAGAATGAAGGAGCGGGGTTTACGGAGCGGACTGTG	1254	Db	2218	GTTCCTTTAAAGACTGGTTGGCTATGCGCAAGGCTATTAGAGCGCATACCCGGAAGT	2277
QY	1315	CTGGAGTTTGAAGGAAATTCAGATGCTGTGGCTTCATGACCTTCGTCAAGCAGTAC	1374	QY	2395	ACCCCGGAGGAGCGCTCTCTCGACAAGCAACAGCGCGCATCAAGTGGTGTGCAAC	2454
Db	1255	CTGGAGTTTGTAGTAGTAATTCAGAGTATTAATTTGCAATTTATGACCTCGTAAACAGTAC	1314	Db	2278	TCCTCAGATGAAGCAGTGTATTAGACAAACAAAGCCCGGATATAAGTAGTTTGTAT	2337
QY	1375	GGCCCGGAGTTCGTGACCGGTTACACATCATCACTTCGACTGGCCCTTCGCTCGACC	1434	QY	2455	TCGGTGTACGGGTTTCAACCGGCGCAGCACGCTCTTCTGCGCTGCTCGCATGTCGCGCC	2514
Db	1315	GCTCCGAGTTTGGCCACAGGTTATACATTTGTAATTTTGTATGGCGTTTATATGGAG	1374	Db	2338	TCCGTGTACGGTTTACTTGGAGTTGCGCAGGATTTCTGCCATGTTTATACGTAGCGCC	2397
QY	1435	AAGCTGACGGAGATCTACAAGGTCCTCGCTCGACGGGTACGGCGCATGAACGGCGGGGT	1494	QY	2515	ACCGTGAACGACATCGGCCGCGAGATGCTCTCTCGCAGCGCGCGCTACGTGACCGCGCG	2574
Db	1375	AACTTAATTTATATACAGTCTCAAGCTTGATGTATGGCAGTATAAACCGTGGGGT	1434	Db	2398	ACTGTCACTACAAATTTGGCCGTCAAATGTTATTAAGTACAGAGATTATATCATATAAC	2457
QY	1495	GTGTTCCGGTGTGGACATCGGCGCAGAGCCACTTTTCAAGACGCGCAGCAAGATCAAGTG	1554	QY	2575	TGGCGGAGTTTCACTGCTGCGACCTTTCGGH--GGCGCGCGCATGCGCGCC	2631
Db	1435	CTGTTTAAGATATGGGATGTGGCAATCCGGATTTCAAGCAAGCAAGGTTAAAGATC	1494	Db	2458	TGGCGCGCATTTGAACGTTTATTAACGCGTTTTCAGACATTTGAAGTAGCGTTCTCTCC	2517
QY	1555	AAGGGATGGTGAACATCGACATGTACGGCATCATCACCGACAGGTCAACTCTCCAGC	1614	QY	2632	CCCGTCCGTACTCCATCGCATCATCTACGGGGACAGGACTCCATTTTTCGTTTGTGC	2691
Db	1495	AACGGTCTCATATCTCTGGATATGATGCAATTTGCAACTGAAAAATTAACCTCTCGAGT	1554	Db	2518	CAAAAGGCTACGAGGTAAGGTTATATATGGAGATACGGATTCTGTATTATCCGATTC	2577
QY	1615	TACAAGCTGAACCGCTCGCGAGGCGCTTTGAAGGACAAAGAAAGGATCTGAGCTAC	1674	QY	2692	CGCGCTTACGCGCGCGGCTGGTGGCCATGGCGCAAGAGATGGCGAGCCACATCTCG	2751
Db	1555	TATAAATTAGATTCGGTTGCACTGAGCTCTAATAGCTCCAGAGAGATTTGCCCTAC	1614	Db	2578	AAGGGTGTAGTTGTAGGGGATAGTAAATTCGGCGAGAAAAATGGCACAATATAATTCA	2637
QY	1675	CGCGACATCCCGCTTACTACGCTCCGGCCCGCGACGCGGGGTGATCGCGAGTAT	1734	QY	2752	CGCGCGCTTCTCTCCCGCATCAAGCTCGAGTCGGAAGAAACCTTCAACAGCTGCTG	2811
Db	1615	AAAGACATTCGGGATATTACGCTAGTGACCGAATACACGAGGAATATTGCTGAATAT	1674	Db	2638	ACGGCTGTGTTGTCTCTTATAAAGTTGGAGTGTGAAAAAATTTTATAAAAATTTTG	2697
QY	1735	TGTGTCAGACTCGCTGTGCTGGGAGCTGTCTTCAAGTTTCTCGCGCACCTTGGAG	1794	QY	2812	CTCATCGCAAGAAAAAGTACATCGGCTCATCTCGGGGGCAAGATGCTCATCAAGGCG	2871
Db	1675	TGTATACAAGACTCGGCTCTTGGGGAACTGTTTTTTTAAATATTTTACACACCTTGAG	1734	Db	2698	CTTATAACAAGAAAAAGTACATTTGGGTAATTTACGGGGAAGGTTTTTAATGAAGGA	2757
QY	1795	CTTTCCGCGCTCGCGGCTGGCGGCATCAACATCACCCGCAACCATCTACGACGCGCAG	1854	QY	2872	GTGGATCTGGTGGCAAAAAACAACCTGCGGTTTATCAACCGCACTCCAGGGCCCTGGTC	2931
Db	1735	TTATCCGCGGTTGCAAGGCTAGCTAGAAATTAATTTAACCAAGGCTATTTACGCGGACG	1794	Db	2758	GTCTGATCTGGTTAGAAAAAAACAACCTGTCAAATTTTATAACGATTATGCGCGCAAACTTGA	2817
QY	1855	CAGATCCGCTCTTCAAGTCCCTTCGCGCTTGGCGGCGAAGAGGCTTCATCTCGCG	1914	QY	2932	GACCTGCTGTTTTCAGCATACCTGATTCGGAGCGCGCGCTTAGCCGAGCGCC	2991
Db	1795	CAGGTTAGGATTTACACCTGTTTATTAGGACTGGCTTCGTCGAGGATTTATTTTACCC	1854	Db	2818	GAACTGTGTTTATATGACGACACCGCTCTCGCGTGTGCGGCGGAGCGGCTGCTGTGTTCC	2877
				QY	2992	GCAGGAGAGTGGCTGGCGCGACCCCTGCGCGAGGAGTGTGAGGCGTTTCGGGGCGCTCTC	3051

Db 2878 ATTGCTGAATGAATAGACGGGCATGCCGTCTGGATGCGGGTTTGGACGATAAAT 2937
Qy 3052 GTAGAGCCCATCGGCGCATCACGACCCGGAGAGGACATCCAGACTTTGTCCTACC 3111
Db 2938 GCAGATGCATCGCAGATTATCATCCCAAAATGGATTAATAAGTTTGTATGACG 2997
Qy 3112 GCCAACTGAGCAGACACCCGCGGTACACCAACAAAGCGCTGCGCCACCTGACGGTG 3171
Db 2998 GCCGAGTTAGTGTCCACCATCCGCTACATAAACCGTGTGCTCACTTAAACGTA 3057
Qy 3172 TATTACAGCTCATGGCCCGCGCGAGGTCCGTCCATCAAGACCGGATCCCGTAC 3231
Db 3058 TATTATAAATTAGTAATGACAGAGGTCAATCCCAACGTTCCGAGAACGCATCCCTTAT 3117
Qy 3232 GTGATCGTGCCCGACCCCGCGAGGTAGAGG 3262
Db 3118 GTTATTGTGCCCCCACAGACGAAGTGGAGG 3148

RESULT 15
US-09-661-596A-76/c
; Sequence 76, Application US/09661596A
; Patent No. 6528066
; GENERAL INFORMATION:
; APPLICANT: Santos, Richard
; TITLE OF INVENTION: VARIANT VARICELLA-ZOSTER VIRUSES AND METHODS OF USE
; FILE REFERENCE: 140.0011 0101
; CURRENT APPLICATION NUMBER: US/09/661,596A
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/153,779
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 76
; LENGTH: 124884
; TYPE: DNA
; ORGANISM: Varicella zoster
US-09-661-596A-76

Query Match 18.9%; Score 701.8; DB 4; Length 124884;
Best Local Similarity 53.7%; Pred. No. 1.1e-126;
Matches 1659; Conservative 0; Mismatches 1312; Indels 120; Gaps 5;

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Qy 283 GTCCACGAGCGCGCTCGCGCGCGCCCTTAAAGTGTACTGCGGGGGGACGAGCGGAC 342
Db 50450 GTTCAGTGGTACACTTAGTCGACCGCTTAAAGTTTACTGTAATGGAAGAGTTCCG 50391
Qy 343 GTCTCCGGTGGGCGGAGGGCTTCTGCGCGCGTGTGCGCTGTGGGCGGTGCG 402
Db 50390 ATTCTGGATTTTGTGTTTCCAGCCCTGCGCTAGACGCGTGAATATTTGGGGGAAATC 50331
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Qy	2932	GACCTGCTGTTTATACAGCATACCGTATCCGAGGGCGCGCGCGCTTATAGCGAGCGCCCC	2991
Db	47819	GAACCTGTTGTTATATGACGACACCGTCTCGCGTGTCTCGCGGAGCGCTCGTGTGTTTCC	47760
Qy	2992	GCAGAGAGTGGCTGGCGGACCCCTGCCCCGAGGAGCTGACGGCGTTCGGGGCCGTCCTC	3051
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Qy	3112	GCGCACTGAGCAGACACCCGCGCGGTACACCAAGACGGCCTCGGCCCACTGACGGTG	3171
Db	47639	GCCGAGCTTAGTCTGCCACCATCCGCTTACATAAAACCGTCGCTTGGCTCACTTAACAGTA	47580
Qy	3172	TATTACAAGTCTATGCCCGCGCGGAGGTCCCGTCCATCAAGGACCGGATCCCGTAC	3231
Db	47579	TATTATAAATTAGTAATGAGACGGGTCAATCCCAACGTTTCGAGAACGCATCCCTTAT	47520
Qy	3232	GTGATCGTGCCCGAGACCCGCGAGGTAGAGG	3262
Db	47519	GTTATTGTGCCCCCAAGCAAGTGGAGG	47489

Search completed: August 6, 2005, 09:57:55
Job time : 598 secs

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48962	TGTATACAAGACTCGGCTCTGTGGGAAACTGTCTTTTAAATATATATACCACTCTGAG	48903
1795	CTTTCCGCGCTCGCGGCGCTTGGGGGCATCAACATCACCCGCACCATCTACGACGCCAG	1854
48902	TTATCCGCGGTCGAAGGCTAGCTAGAACTTACTTTAAACCAAGCTATTTACGACGGACAG	48843
1855	CAGATCCGCTCTTACGTGCTCTGCGGCTTGGCGGCCAGAAAGGCTTCAATCTCTGCCG	1914
48842	CAGGTTAGGATTTACACCTGTTTATTAGGACTGGCTTCGCTCGAGGATTTATTTTACCC	48783
1915	GACACCCAGGGCGGTTTCGGGSCCTCGACAAGAGAGGCCCAAGCGGCCGCTGCGCT	1974
48782	GATGGGGATACCAAGCTACTTTTGAATATAAGGATGTTATTC-----	48739
1975	CGGGGGAAAGGGAGCGCGCGGGGACGGGAAACGGGACGAGGATAAGGACGACACGAG	2034
48738	-----CGATGTCGGGATGTTGAGGAA	48717
2035	GACAGGACGGGACAGACGCGAGGAGGTCGCGCGGAGACCGGGGGCGGCACTTTGGG	2094
48716	GAGATGATGAACACGAGAGCGTTCTCCCACTGTGTACGTCAAGTGGGCGAAATGTAGGA	48657
2095	TACCAGGGGCGGGGTCCTGCACCCACCTCTCGGCTTTCACGTGCAGCCCGTGTGTGTG	2154
48656	TATAAGGAGCCAGGGTTTTTGACCTCGATACGGGATTTATCGATCCGGTGTGCTGA	48597
2155	TTTGACTTTGCCAGCCTGTACCCAGCATCATCCAGGCCCAACAACCTGTGCTTCAGTACG	2214
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48359	TCTTCAGATGAAGCAGTGTATTATAGACAAACAACAGCCGCGATAAAGTAGTTGTGAAT	48300
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48239	ACTGTCACTACAATGGCCGTCAAAATGTTATTAAGTACAGAGATTTATTTCAATAATAC	48180
2575	TGGCGGAGTTCCATCAGCTGTGCGGCACTTTCCGGA---GGCGGCCGGCATGCGGCC	2631
48179	TGGGCGCAATTTGAACGTTTTTATCAGCGTTTCCAGACATTTGAAAGTAGCGTCTCTCC	48120
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2692	CGGGCCTCACGGCGCGGCCCTGGTGGCCATCGGGCGACAAGATGGCGAGCCACATCTCG	2751
48059	AAGGTTGTAGTTTNGGGGATAGCTAAATTCGGCGAGAAATGGCACATATAATTCA	48000
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Result	No.	Query			DB	ID	Description
		Score	Match	Length			
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2	2	3717	100.0	3717	6	AK358310	AK358310 Sequence
3	3	3696.2	99.4	3723	6	AR454708	AR454708 Sequence
4	4	3696.2	99.4	3723	6	AK358312	AK358312 Sequence
5	5	3696.2	99.4	3723	14	AY038367	AY038367 Human her
6	6	3694.6	99.4	3723	14	AY038366	AY038366 Human her
7	7	3693	99.4	3723	14	AY038365	AY038365 Human her
8	8	3686.6	99.2	4003	14	HSV2HG52	Z86099 Herpes simp
9	9	3059.8	82.3	3708	6	HS2POL	M16321 HSV-2 DNA p
10	10	3059.8	82.3	3708	6	AK354709	AK354709 Sequence
11	11	3059.8	82.3	3708	6	AK358314	AK358314 Sequence
12	12	3058.2	82.3	3708	14	AB070847	AB070847 Human her
13	13	3056.6	82.2	4435	14	AB070848	AB070848 Human her
14	14	3053.4	82.1	3708	6	HS1POL	M10792 Herpes simp
15	15	3053.4	82.1	3708	6	AR454710	AR454710 Sequence
16	16	3053.4	82.1	3708	14	AK358316	AK358316 Sequence
17	17	3048.6	82.0	3708	6	HEHSV1DP	X04771 Herpes simp
18	18	3048.6	82.0	3708	14	AB072389	AB072389 Human her
19	19	3047	82.0	152261	14	HE1CG	X14112 Human herpe
20	20	3047	82.0	3708	6	AR454711	AR454711 Sequence

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Db 301 CGCGCCGCCCTTAAGGTGTACTCGCGGGGGGAGCGAGCGCAGCTTCCTCCCGTGGGCGCG 360
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DB 3421 CTGGTGTCCGAGTGGCGGAGATCCCGGATACCGCATCGCGCGGCGCTTCCGCTCAAC 3480
QY 3481 ACAGACTATTACTTCTCGACCTGCTGCGGCGCGCTGCGTGAGCTTCAAGGCCCTGTTT 3540
DB 3481 ACAGACTATTACTTCTCGACCTGCTGCGGCGCGCTGCGTGAGCTTCAAGGCCCTGTTT 3540
QY 3541 GGAATAACCGCAAGATCACCGAGAGTCTGTTTAAAGAGGTTTATTTCCCGAGAGCGTGGCAC 3600

DB 3541 GGAATAACCGCAAGATCACCGAGAGTCTGTTTAAAGAGGTTTATTTCCGAGAGCGTGGCAC 3600
QY 3601 CCCCCGACACAGTGGCGCGGCTCAGCGCGCGCGGGTTCGGGCCCGCGGGCGCGGCG 3660
DB 3601 CCCCCGACACAGTGGCGCGGCTCAGCGCGCGCGGGTTCGGGCCCGCGGGCGCGGCG 3660
QY 3661 GCTACGGCGAGGAAACTCGTCCGAATGTCATAGAGCTTTGATACTCTTAGCATGA 3717
DB 3661 GCTACGGCGAGGAAACTCGTCCGAATGTCATAGAGCTTTGATACTCTTAGCATGA 3717

RESULT 2
AX358310
LOCUS 3717 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 1 from Patent WO0206513.
ACCESSION AX358310
VERSION AX358310.1 GI:18674960
SOURCE Human herpesvirus 2
ORGANISM Human herpesvirus 2
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.

REFERENCE
1
AUTHORS Homa, F.L., Wathen, M.W., Hopkins, T.A. and Thomsen, D.R.
TITLE A method for treating herpes viruses
JOURNAL Patent: WO 0206513-A 1 24-JAN-2002;
PHARMACIA & UPJOHN COMPANY (US)

FEATURES
source
1. 3717
/organism="Human herpesvirus 2"
/mol_type="unassigned DNA"
/db_xref="taxon:10310"
/note="DNA polymerase"

ORIGIN

Query Match 100.0%; Score 3717; DB 6; Length 3717;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTTGTGCGCGGCGCGCGCTTCCCGGGGGGAGTCTCGCGGCTCGGCGGCG 60
DB 1 ATGTTTGTGCGCGGCGCGCGCTTCCCGGGGGGAGTCTCGCGGCTCGGCGGCG 60
QY 61 TCTGGGTTTTTTCG 120
DB 61 TCTGGGTTTTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 121 CGCGCGCAGAACTTCTACAAACCCCGCTCAGACCGGAAACGAGCGCGCGCG 180
DB 121 CGCGCGCAGAACTTCTACAAACCCCGCTCAGACCGGAAACGAGCGCGCG 180
QY 181 GGGCGGCTCAGCGCGCATAGTACTACGAGAGTGGACGAAATTCGATTTTCGCG 240
DB 181 GGGCGGCTCAGCGCGCATAGTACTACGAGAGTGGACGAAATTCGATTTTCGCG 240
QY 241 CGTTCTGTCGACGAGACGCGCGCGGAGCGCGCGCGGTTCCACGACGCGCGCTC 300
DB 241 CGTTCTGTCGACGAGACGCGCGCGGAGCGCGCGCGGTTCCACGACGCGCGCTC 300
QY 301 CGCGCGCGCGCTTAAGGTGTACTGCGGGGGGAGCGAGCGAGACGCTCTCCGCTGGGCG 360
DB 301 CGCGCGCGCGCTTAAGGTGTACTGCGGGGGGAGCGAGCGAGACGCTCTCCGCTGGGCG 360
QY 361 GAGGGCTTTCGCGCGCTGCTTGGCGGCTGTCGGAGCGGTTCGCGACCATGCCCCCAAGGG 420
DB 361 GAGGGCTTTCGCGCGCTGCTTGGCGGCTGTCGGAGCGGTTCGCGACCATGCCCCCAAGGG 420
QY 421 TTTCGACCCCGTTCACCGCTTTCACGCTGTCAGACATCTCTGGAGCAGCTGGGACACGCG 480
DB 421 TTTCGACCCCGTTCACCGCTTTCACGCTGTCAGACATCTCTGGAGCAGCTGGGACACGCG 480
QY 481 TACAGCATGCGCGCGCGCGCGCTTCCACGAGCGATTTATGGACGCCATTCACGCGCGCG 540

Db	481		TACAGCATGCGCGCCAGCTCCACGAGCGATTTATGACGCCATCAACGCCGCGCGG	540
Qy	541		ACCGTATACAGCTTCTGGGTCTGACCCCGAAGGCCATCGCTCGCGCTTCAAGTCTAC	600
Db	541		ACCGTATACAGCTTCTGGGTCTGACCCCGAAGGCCATCGCTCGCGCTTCAAGTCTAC	600
Qy	601		GGCAGCGGCGAGTACTTTTATCATGAACAAGCGGAGGTGATCGGCACCTGCAAGTGCCT	660
Db	601		GGCAGCGGCGAGTACTTTTATCATGAACAAGCGGAGGTGATCGGCACCTGCAAGTGCCT	660
Qy	661		GCCCGCGCGATCTCTCGAGCGCTTGGCGCGCGCCCTGCGAGTGCCTCGCGCGGTGCG	720
Db	661		GCCCGCGCGATCTCTCGAGCGCTTGGCGCGCGCCCTGCGAGTGCCTCGCGCGGTGCG	720
Qy	721		TTCCGCGCGATCTCCGCGGACCACTTCGAGCGGAGGTGATGAGCGCGCGAGTGTATC	780
Db	721		TTCCGCGCGATCTCCGCGGACCACTTCGAGCGGAGGTGATGAGCGCGCGAGTGTATC	780
Qy	781		TATTACGAAGCGCGCCGACCTCTGACTACCGGCTTCTGTCGAAAGCGGCGCGGCTG	840
Db	781		TATTACGAAGCGCGCCGACCTCTGACTACCGGCTTCTGTCGAAAGCGGCGCGGCTG	840
Qy	841		GCCTACCTGTGCGACAACTTTTGGCCCGCGATCAGGAAGTACGAGGCGGCGCTCGACGC	900
Db	841		GCCTACCTGTGCGACAACTTTTGGCCCGCGATCAGGAAGTACGAGGCGGCGCTCGACGC	900
Qy	901		ACCAACCGGTTTATCTGGACCAACCCCGGGGTTTGTACCTTCGGCTGGTACCGCTCAAG	960
Db	901		ACCAACCGGTTTATCTGGACCAACCCCGGGGTTTGTACCTTCGGCTGGTACCGCTCAAG	960
Qy	961		CCGCGCGCGGAAACCGCGCCCAACCGCGCCCGCGGCTTTCGGAACCTCGAGC	1020
Db	961		CCGCGCGCGGAAACCGCGCCCAACCGCGCCCGCGGCTTTCGGAACCTCGAGC	1020
Qy	1021		GAGTCTGAGTTTAACTGCAAGCGGCAAACTGCGCGTCAAGGCGGCGATGTGTACCTG	1080
Db	1021		GAGTCTGAGTTTAACTGCAAGCGGCAAACTGCGCGTCAAGGCGGCGATGTGTACCTG	1080
Qy	1081		CCGCGCTTACAGCTCATGCTTTCGATATCGAATGCAAGCGCGGCGGAGGACGAGCTG	1140
Db	1081		CCGCGCTTACAGCTCATGCTTTCGATATCGAATGCAAGCGCGGCGGAGGACGAGCTG	1140
Qy	1141		GCCTTTCCGGTTCGCGGAAACCGCGGAGACTTCTCATCCAGATCTCTCTGCTCTAC	1200
Db	1141		GCCTTTCCGGTTCGCGGAAACCGCGGAGACTTCTCATCCAGATCTCTCTGCTCTAC	1200
Qy	1201		GACCTGTCCACCGCCCTCGAGCACATCTCTGTTTTCGCTCGGATCTCTGCGACCTC	1260
Db	1201		GACCTGTCCACCGCCCTCGAGCACATCTCTGTTTTCGCTCGGATCTCTGCGACCTC	1260
Qy	1261		CCGAGTCCACCTTCAGGATCTCGCTCCAGGGGCTCGCGCCCGCTCGCTCGGAG	1320
Db	1261		CCGAGTCCACCTTCAGGATCTCGCTCCAGGGGCTCGCGCCCGCTCGCTCGGAG	1320
Qy	1321		TTTGACAGCGAATTCGAGATGCTGCTGCGCTTATGACCTTTCGTAAGCAGTACGCGCC	1380
Db	1321		TTTGACAGCGAATTCGAGATGCTGCTGCGCTTATGACCTTTCGTAAGCAGTACGCGCC	1380
Qy	1381		GAGTTCGTGACCGGGTCAACATCATCAACTTCGACTGGGCTTTCGCTTCGACCAAGCTG	1440
Db	1381		GAGTTCGTGACCGGGTCAACATCATCAACTTCGACTGGGCTTTCGCTTCGACCAAGCTG	1440
Qy	1441		ACGAGATCTACAGGTCCTCGAGGTACGGGCGCATGAACCGCGGGGTGTTC	1500
Db	1441		ACGAGATCTACAGGTCCTCGAGGTACGGGCGCATGAACCGCGGGGTGTTC	1500
Qy	1501		CGCGTGTGGACATCGGCGCAGAGCACTTTTCAAGCGCAGCAAGATCAAGGTGAACGGG	1560
Db	1501		CGCGTGTGGACATCGGCGCAGAGCACTTTTCAAGCGCAGCAAGATCAAGGTGAACGGG	1560
Qy	1561		ATGCTGAACATCGACATGTACGGCATCATCAACGAGCAAGGTCAAACTCTCCAGTCAAG	1620
Db	1561		ATGCTGAACATCGACATGTACGGCATCATCAACGAGCAAGGTCAAACTCTCCAGTCAAG	1620
Qy	1621		CTGAAACCGCGTTCGAGGCGCGTCTTGAAGGCAAGAAAGGATCTGAGCTACCGCGAC	1680
Db	1621		CTGAAACCGCGTTCGAGGCGCGTCTTGAAGGCAAGAAAGGATCTGAGCTACCGCGAC	1680
Qy	1681		ATCCCGCCTACTACGCTTCGCGGCGCGAGCGCGGGTGTATCGCGAGTATTGTGTG	1740
Db	1681		ATCCCGCCTACTACGCTTCGCGGCGCGAGCGCGGGTGTATCGCGAGTATTGTGTG	1740
Qy	1741		CAGGACTCGCTGTGTGTCGGGCGAGTCTTCAAGTTTCTGCGGCACTTGGAGCTTTTC	1800
Db	1741		CAGGACTCGCTGTGTGTCGGGCGAGTCTTCAAGTTTCTGCGGCACTTGGAGCTTTTC	1800
Qy	1801		GCGCTCGCGCTGTCGGGCGCATCAACATCACCCGACCATCTACGAGCGCGAGCAGATC	1860
Db	1801		GCGCTCGCGCTGTCGGGCGCATCAACATCACCCGACCATCTACGAGCGCGAGCAGATC	1860
Qy	1861		CGGCTCTTCACTGCTTCTGCGCTTTCGCGGCGCGAGGCTTCACTTCGCGGCAACC	1920
Db	1861		CGGCTCTTCACTGCTTCTGCGCTTTCGCGGCGCGAGGCTTCACTTCGCGGCAACC	1920
Qy	1921		CAGGCGCGTTCGCGGCGCTCGAAGAGGCGCGCCCAAGCGCGCGCTCGCGG	1980
Db	1921		CAGGCGCGTTCGCGGCGCTCGAAGAGGCGCGCCCAAGCGCGCGCTCGCGG	1980
Qy	1981		GAGGCGGAGCGCGCGGCGCATCAAGGAGCGAGGATAAGGACGACGAGGAGCGAG	2040
Db	1981		GAGGCGGAGCGCGCGGCGCATCAAGGAGCGAGGATAAGGACGACGAGGAGCGAG	2040
Qy	2041		GACGCGGAGCGCGGAGGCTGCGCGCGAGACCGCGGCGCGGACGCTTGGGTACCG	2100
Db	2041		GACGCGGAGCGCGGAGGCTGCGCGCGAGACCGCGGCGCGGACGCTTGGGTACCG	2100
Qy	2101		GCGGCGCGGCTCTCGACCCCTCGCGGTTTCACTGCGGCTTCACTGCTCTCTCTCT	2160
Db	2101		GCGGCGCGGCTCTCGACCCCTCGCGGTTTCACTGCGGCTTCACTGCTCTCTCTCT	2160
Qy	2161		TTTGCGAGCTGTACCCCGAGCATCTCAGGCGCGCAAACTGCTCTTCACTGCTCTCT	2220
Db	2161		TTTGCGAGCTGTACCCCGAGCATCTCAGGCGCGCAAACTGCTCTTCACTGCTCTCT	2220
Qy	2221		CTGCGCGCGAGCGCTGCGCACCTGAGGCGGACCGGCGACTTCTGAGATCGAGGTG	2280
Db	2221		CTGCGCGCGAGCGCTGCGCACCTGAGGCGGACCGGCGACTTCTGAGATCGAGGTG	2280
Qy	2281		GCGGCGCGAGCGCTGCTTCTGTAAGCGCGCATGAGGCGCGGCGCTGAGCATCTCT	2340
Db	2281		GCGGCGCGAGCGCTGCTTCTGTAAGCGCGCATGAGGCGCGGCGCTGAGCATCTCT	2340
Qy	2341		CTGCGGACTTGGCTGCGCATCGAAGCAGATCCGCTCGCGATCCCGCAGAGCACCCC	2400
Db	2341		CTGCGGACTTGGCTGCGCATCGAAGCAGATCCGCTCGCGATCCCGCAGAGCACCCC	2400
Qy	2401		GAGGAGCGCTCTCTCGCAAGCAACAGCGCGCGCATCAAGGTGTGTGCAACTCGGTG	2460
Db	2401		GAGGAGCGCTCTCTCTCGCAAGCAACAGCGCGCGCATCAAGGTGTGTGCAACTCGGTG	2460
Qy	2461		TACGCGTTCAACCGGCGCGAGCATCGGTCTTCTGCGCGCTGCACTGCGCGCGACCG	2520
Db	2461		TACGCGTTCAACCGGCGCGAGCATCGGTCTTCTGCGCGCTGCACTGCGCGCGACCG	2520
Qy	2521		ACGACCATCGCGCGCGAGATGCTTCTCGGCAACCGCGCGCTTACGTGACGCGCTGGCG	2580
Db	2521		ACGACCATCGCGCGCGAGATGCTTCTCGGCAACCGCGCGCTTACGTGACGCGCTGGCG	2580
Qy	2581		GAGTTCGATCAGCTGTGCGCGACTTTTCGAGGCGCGCGCATGCGCGCCCCCGGTCCG	2640
Db	2581		GAGTTCGATCAGCTGTGCGCGACTTTTCGAGGCGCGCGCATGCGCGCCCCCGGTCCG	2640
Qy	2641		TACTCCATCGCATCATCTACGGGAGACGAGCTCCATTTTCTGTTTGTGCGCGGCTC	2700
Db	2641		TACTCCATCGCATCATCTACGGGAGACGAGCTCCATTTTCTGTTTGTGCGCGGCTC	2700

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Qy 2995 GAGGAGTGGCTGGCGGACACCTCTGCCGAGGAGATGACAGGCGTTTCGGGGCGCTCTCGTA 3054
Db 3001 GAGGAGTGGCTGGCGGACACCTCTGCCGAGGAGATGACAGGCGTTTCGGGGCGCTCTCGTA 3060
Qy 3055 GACGCCATCGCGGATACCGACCCGAGAGAGGACATCCAGGACTTTGTCCTCACCGCC 3114
Db 3061 GACGCCATCGCGGATACCGACCCGAGAGGAGACATCCAGGACTTTGTCCTCACCGCC 3120
Qy 3115 GAACTGAGCAGACACCGCGCGCTACACCAACGCGCTGCGCCACCTGACGGTGTAT 3174
Db 3121 GAACTGAGCAGACACCGCGCGCTACACCAACGCGCTGCGCCACCTGACGGTGTAT 3180
Qy 3175 TACAAGTCTATGGCCCGCGCGCGAGTCCCGTCCATCAAGGACCGGATCCCGTAGCTG 3234
Db 3181 TACAAGTCTATGGCCCGCGCGAGTCCCGTCCATCAAGGACCGGATCCCGTAGCTG 3240
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Db 3241 ATCTGGCCAGACCCCGGAGGTAGAGAGACGTCGCGGCTGGCGCCCTCCGCGAG 3300
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Qy 3355 AAGCGCCCGCGGAGAGCGCTGCGATGCGGACCGCCCGCGGAGCGGCTCCAGCCCGC 3414
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Qy 3415 AAGCTGCTGTGTCGAGTGGCGAGGATCCCGGTCAGCATCGCCCGGGGGGTTCCG 3474
Db 3421 AAGCTGCTGTGTCGAGTGGCGAGGATCCCGGTCAGCATCGCCCGGGGGGTTCCG 3480
Qy 3475 CTAAACAGGACTATTCTCTCGACCTGCTGGGGGGGCGCTCGGTGACGTTCAAGGCC 3534
Db 3481 CTAAACAGGACTATTCTCTCGACCTGCTGGGGGGGCGCTCGGTGACGTTCAAGGCC 3540
Qy 3535 CTGTTTGGAAATACGCAAGTACCGAGAGTCTGTTAAAGAGTTTATTCCCGGAGCG 3594
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Db 3601 TGGCACCCCGCGAGCGTGGCGCGCGCTCAGGGCCGCGGGTTCGGGCGCGCGGG 3660
Qy 3655 GCGGGCGCTACGGCGGAGGAACTCTGTCGAATGTGTCATAGAGCGCTTTGATCTAGCA 3714
Db 3661 GCGGGCGCTACGGCGGAGGAACTCTGTCGAATGTGTCATAGAGCGCTTTGATCTAGCA 3720
Qy 3715 TGA 3717
Db 3721 TGA 3723

RESULT 4
AX358312
LOCUS AX358312 3723 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 3 from Patent WO0206513.
ACCESSION AX358312
VERSION AX358312.1 GI:18674961
KEYWORDS
SOURCE Human herpesvirus 2 strain 186
ORGANISM Human herpesvirus 2 strain 186
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
REFERENCE 1
Homa, F.L., Wathen, M.W., Hopkins, T.A. and Thomeen, D.R.
A method for treating herpes viruses
Patent: WO 0206513-A 3 24-JAN-2002;
PHARMACIA & UPJOHN COMPANY (US)
FEATURES
Location/Qualifiers
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source

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ORIGIN

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 3714; Conservative 0; Mismatches 3; Indels 6; Gaps 1;
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Qy 61 TCTGGGTTTTTGGCCCCCAACACCCCGGGGAGCCACCCAGAGCGCACCGCCGCTTTCG 120
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Qy 121 CGCGCGGAGAACTTCTAAACACCCCACTCTCGCTCAGACCGGAAACGAGCCCAAGCC 180
Db 121 CGCGCGGAGAACTTCTAAACACCCCACTCTCGCTCAGACCGGAAACGAGCCCAAGCC 180
Qy 181 GGGCGGCTCAGCGCCATACGTACTACGAGAGTGCAGCAATTTTCGATTTATCGCCCG 240
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Qy 241 CGTTCCGTGAGAGGAGCGCCCGCGGAGCGAGCGACCGGGTTCACGACGGCGCGCTC 300
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Qy 361 GAGGGCTTTCGCGCGCTGCTGCGCTTGGGGCGGTGCGGACCATATGCCCCCAAGGG 420
Db 361 GAGGGCTTTCGCGCGCTGCTGCGCTTGGGGCGGTGCGGACCATATGCCCCCAAGGG 420
Qy 421 TTGACCCCCACGCTCACCGCTTTCAGCTGTACGACATCTTGGAGACGCTGGAACACGCG 480
Db 421 TTGACCCCCACGCTCACCGCTTTCAGCTGTACGACATCTTGGAGACGCTGGAACACGCG 480
Qy 481 TACAGCATGCGCGCCCGCCAGCTCCAGCGAGTATTTATGACGCCATCAAGCCCGCGGG 540
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Qy 541 ACCGTATACGCTTCTGGGTCTGACCCCGAAGGCCATCGCGTTCGCGCTTACGTCTAC 600
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Qy 601 GGCACGGCGAGTACTTTTACATGAACAGCGGAGGTGATCGGACCTGCGAGTGGCGGT 660
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Qy 661 GCGCGCGCGATCTCTCGAGCGCTTGGCGCGCGCTTGGCGAGTCCGCGGGGGCGTTCG 720
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Qy 781 TATTACGAACGCGCGGACCTTGTACTACCGGCTTTCGTCGAGAGCGGGCGCGCGCTG 840
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Qy 901 ACCACCGGTTTATCTCGGACAAACCGGGGTTTGTACCTTTCGGCTGGTACCGCTCAAG 960
Db 901 ACCACCGGTTTATCTCGGACAAACCGGGGTTTGTACCTTTCGGCTGGTACCGCTCAAG 960

QY	961	CCCCCGCGGGAACGCGCGGCGCAACCGCGCCCGCCCGCGGCTTCGGAACTCTGAGC	1020
Db	961	CCCCCGCGGGAACGCGCGGCGCAACCGCGCCCGCCCGCGGCTTCGGAACTCTGAGC	1020
QY	1021	GACGTCAGGTTTAACTGCAAGGCGGCAAACTGCGCTCGAGGGGGCCATGTGTGACCTG	1080
Db	1021	GACGTCAGGTTTAACTGCAAGGCGGCAAACTGCGCGCTCGAGGGGGCCATGTGTGACCTG	1080
QY	1081	CGGCGCTACAGCTCATGTCTCGATATCGAATGCAAGCGCGGGGGGAGGAGAGCTG	1140
Db	1081	CGGCGCTACAGCTCATGTCTCGATATCGAATGCAAGCGCGGGGGGAGGAGAGCTG	1140
QY	1141	GCCTTTCCGGTTCGCGGAAGCGCGGGAAGACTCGTCAATCCAGATCTCTCTGTCTGTAC	1200
Db	1141	GCCTTTCCGGTTCGCGGAAGCGCGGGAAGACTCGTCAATCCAGATCTCTCTGTCTGTAC	1200
QY	1201	GACCTGTCCACACCGCGCTCGAGCAATCCTCTGTGTTTTCGTTCGGATCCTCGACCTC	1260
Db	1201	GACCTGTCCACACCGCGCTCGAGCAATCCTCTGTGTTTTCGTTCGGATCCTCGACCTC	1260
QY	1261	CCGAGTCCACCTCAGCGATCTCGCTCCAGGGGCTCGCGGCCCGCTCGCTGGAG	1320
Db	1261	CCGAGTCCACCTCAGCGATCTCGCTCCAGGGGCTCGCGGCCCGCTCGCTGGAG	1320
QY	1321	TTTGACAGCGAATTCGAGATGCTGTGGCTTCATGACCTTCGTCAAGCAGTAGTACGGCCCC	1380
Db	1321	TTTGACAGCGAATTCGAGATGCTGTGGCTTCATGACCTTCGTCAAGCAGTAGTACGGCCCC	1380
QY	1381	GAGTTCGTGACCGGGTCAACATCATCAACTTCGACTGGCCCTTCGTCTCGTCAACAGCTG	1440
Db	1381	GAGTTCGTGACCGGGTCAACATCATCAACTTCGACTGGCCCTTCGTCTCGTCAACAGCTG	1440
QY	1441	ACGAGATCTACAAGTCCCGCTCGACGGGTACGGGCGCATGAACGGCGGGGTGTGTTT	1500
Db	1441	ACGAGATCTACAAGTCCCGCTCGACGGGTACGGGCGCATGAACGGCGGGGTGTGTTT	1500
QY	1501	CGGCTGTGGGACATCGGCGCAGAGCACTTTCAGAAAGCGCAGCAAGATCAAGGTGAACGG	1560
Db	1501	CGGCTGTGGGACATCGGCGCAGAGCACTTTCAGAAAGCGCAGCAAGATCAAGGTGAACGG	1560
QY	1561	ATGCTGAACATCGACATGTACGGCATCATCAACGCAAGGTCAAACTCTCCAGCTACAAG	1620
Db	1561	ATGCTGAACATCGACATGTACGGCATCATCAACGCAAGGTCAAACTCTCCAGCTACAAG	1620
QY	1621	CTGAACCCGCTGCGCGGCGGCTTTCAGAGCAAGAGAGGATCTGAGCTACCGGAC	1680
Db	1621	CTGAACCCGCTGCGCGGCGGCTTTCAGAGCAAGAGAGGATCTGAGCTACCGGAC	1680
QY	1681	ATCCCGCGCTACTACGCTCCGGGCGCGCAGCGGGGTGATCGGCGAGTATTTGTGTG	1740
Db	1681	ATCCCGCGCTACTACGCTCCGGGCGCGCAGCGGGGTGATCGGCGAGTATTTGTGTG	1740
QY	1741	CAGACTCTGCTGTGTCGGGAGCTGTTCTTCAAGTTTTCGCGCACTTGGAGCTTTTC	1800
Db	1741	CAGACTCTGCTGTGTCGGGAGCTGTTCTTCAAGTTTTCGCGCACTTGGAGCTTTTC	1800
QY	1801	GCGTTCGCGCGCTGGCGGCATCAACATCACCGCACCATCTACGACGCCAGCAGATC	1860
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QY	1861	CGGCTCTTACGTGCTCTCTCGCTTCGCGGCGCAGAAAGGCTTCATCTTCGCGGACCC	1920
Db	1861	CGGCTCTTACGTGCTCTCTCGCTTCGCGGCGCAGAAAGGCTTCATCTTCGCGGACCC	1920
QY	1921	CAGGGCGGTTTCGGGCGCTTCGACAGAGCGCGCCAAAGCGCGCGCTGCTTCGGGG	1980
Db	1921	CAGGGCGGTTTCGGGCGCTTCGACAGAGCGCGCCAAAGCGCGCGCTGCTTCGGGG	1980
QY	1981	GAAGGGAGCGCGCGGGGACGGGAACGGGACGAGGATGAAGGACGACGACGA-----G	2034
Db	1981	GAAGGGAGCGCGCGGGGACGGGAACGGGACGAGGATGAAGGACGACGACGACGCGG	2040

QY	2035	GACGAGACGGGACGAGCGCGAGAGGTGCGCGGAGACCGGGGGCCCGACGTTGGG	2094
Db	2041	GACGAGACGGGACGAGCGCGAGAGGTGCGCGGAGACCGGGGGCCCGACGTTGGG	2100
QY	2095	TACACGGGGCCCGGGTCTCTGACCCCACTTCGGGTTTCAAGTCACCCCTGTTGGTG	2154
Db	2101	TACACGGGGCCCGGGTCTCTGACCCCACTTCGGGTTTCAAGTCACCCCTGTTGGTG	2160
QY	2155	TTTGACTTTGCCAGCTGTACCCAGCATCATCCAGGCCCAACAACTGTGCTTCAGTACG	2214
Db	2161	TTTGACTTTGCCAGCTGTACCCAGCATCATCCAGGCCCAACAACTGTGCTTCAGTACG	2220
QY	2215	CTCTCCCTCGGGCCCGAGCCGCTCGCGCACCTTGGAGCGGACCGGGAGATC	2274
Db	2221	CTCTCCCTCGGGCCCGAGCCGCTCGCGCACCTTGGAGCGGACCGGGAGATC	2280
QY	2275	GAGGTGGGGGCGGACGGCTTCTTCTGTAAGGCCCAAGTACGCGAGAGCTGTGAGC	2334
Db	2281	GAGGTGGGGGCGGACGGCTTCTTCTGTAAGGCCCAAGTACGCGAGAGCTGTGAGC	2340
QY	2335	ATCTCTCTCGGACCTGGGCTTGGCCATGCGAAAGCAGATCCGCTCGCGGATCCCCAGAGC	2394
Db	2341	ATCTCTCTCGGACCTGGGCTTGGCCATGCGAAAGCAGATCCGCTCGCGGATCCCCAGAGC	2400
QY	2395	ACCCCGGAGGAGCCGCTCTCTCGAAGAACAAAGCGCGCCATCAAGGTGTGTGCAAC	2454
Db	2401	ACCCCGGAGGAGCCGCTCTCTCGAAGAACAAAGCGCGCCATCAAGGTGTGTGCAAC	2460
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J. Gen. Virol. 71 (Pt 6), 1387-1390 (1990)
MEDLINE 90278430
PUBMED 2161906
REFERENCE 3 (bases 1 to 154746)
AUTHORS McGeoch,D.J., Cunningham,C., McIntyre,G. and Dolan,A.
TITLE Comparative sequence analysis of the long repeat regions and
adjoining parts of the long unique regions in the genomes of herpes
simplex viruses types 1 and 2
J. Gen. Virol. 72 (Pt 12), 3057-3075 (1991)
MEDLINE 92113549
PUBMED 1662697
REFERENCE 4 (bases 1 to 154746)
AUTHORS Barnett,B.C., Dolan,A., Telford,E.A., Davison,A.J. and McGeoch,D.J.
TITLE A novel herpes simplex virus gene (UL49A) encodes a putative
membrane protein with counterparts in other herpesviruses
J. Gen. Virol. 73 (Pt 8), 2167-2171 (1992)
MEDLINE 92356101
PUBMED 1322965
REFERENCE 5
AUTHORS Dolan,A.
TITLE Direct Submission
SUBMITTED (25-FEB-1997) A. Dolan, MRC Virology Unit, Church
Street,, Glasgow,, G11 5JR, UK
REMARK revised bu [6]
REFERENCE 6 (bases 1 to 154746)
AUTHORS Dolan,A.
TITLE Direct Submission
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Street,, Glasgow,, G11 5JR, UK
COMMENT On Dec 13, 1999 this sequence version replaced gi:1869820.
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Tsurumi, T., Maeno, K. and Nishiyama, Y.			
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3955 TGA 3957

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AR454709	DEFINITION	Sequence 5 from patent US 6682892.					
AR454709	ACCESSION	AR454709					
AR454709.1	VERSION	AR454709.1	GI:42688213				
KEYWORDS	KEYWORDS	Unknown.					
SOURCE	SOURCE	Unknown.					
ORGANISM	ORGANISM	Unclassified.					
REFERENCE	REFERENCE	1 (bases 1 to 3708)					
AUTHORS	AUTHORS	Homa, F.L., Wathen, M.W., Hopkins, T.A. and Thomsen, D.R.					
TITLE	TITLE	Method for treating herpes viruses					
JOURNAL	JOURNAL	Patent: US 6682892-A 5 27-JAN-2004;					
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source	source	1..3708					
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ORIGIN	ORIGIN	/mol_type="genomic DNA"					
Query Match	Query Match	82.3%; Score 3059.8; DB 6; Length 3708;					
Best Local Similarity	Best Local Similarity	89.3%; Pred. No. 0;					
Matches 3321; Conservative	Matches 3321; Conservative	0; Mismatches 387; Indels 9; Gaps 2;					
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Qy	61	TCGTGGGTTTTGTGCCCCCACA	CCCCCGGGGAGCCACCAGACGGCACCGCCCTTGC	120			
Db	61	TCGGGTTTTGTGCGCCGCGGCC	CTCGGGAGCCGGCC---GGGAGCCCCCGCTTGT	117			
Qy	121	CGCGGGCAGAACTTTCTAAAC	CCCCCACCCTCGCTCAGACCGGAAACGAGCCCAAGGCC	180			
Db	118	TTGAGGCAAAACTTTTACAC	CCCCCTACTCGCCCCAGTCGGGACGCAACAGAAGCCGACC	177			
Qy	181	GGGCGGCTCAGCGCCATAGTA	CTACAGCGAGTGGCAGCAATTTGATTTATCGCCCGG	240			
Db	178	GGGCAACCCAGCGCCCATAG	CTATAGCGAATTCGATGAATTCGATTCATCGCCCGG	237			
Qy	241	CGTTGCTGGACGAGGACGCC	CCCCCGGAGCAGCGCAACCGGGTCCACGCGCGCGCTC	300			
Db	238	CGGTGCTGGACAGGATGAT	CCCCCCCCGGAGAACGCGCGGGGTGCACAGCGTCACTC	297			
Qy	301	CGCGCGCCCTTAAGGTGTACT	TCGGGGGGGACGAGCGCAGCTCTCCGGTGGGCGCG	360			
Db	298	AAGCGCGCCCAAGGTGTACT	TCGGGGGGGACGAGCGAGCTCTCCGGTGGGTGCG	357			
Qy	361	GAGGGCTTTCGCGCGTTCGCT	TGCGCTGTGGGGCGGTGGGACCATATGCCCCCAAGGG	420			
Db	358	GGCGGCTTCTGGCGCGCGCT	CGCGCTGTGGGGCGCGTGGACCAACGCCCGCGCGGG	417			
Qy	421	TTGCACCCACCGTCACGGT	CTTCCAGTGTACCACTCTCGGAGCAGTGGGAACAGCG	480			
Db	418	TTCAACCCCAACCGTCA	CCGCTTTTTCAGTGTACACATCTCTGGAGACGCTGGAGACAGCG	477			
Qy	481	TACAGCATGCGCGCGCCAG	CTCCACGAGCGATTTATGGACGCCATCAGCCCGCGCGG	540			
Db	478	TACGGCATGCGCGCGCCAG	TTTCCACGCGGGTTTATGGACGCCATCACAACGACGGGG	537			
Qy	541	ACCGTCATCAGCTTCTGGG	TCTGACCCCCCGAAGGCCATCGCGTCGCGGTTTACGCTTAC	600			
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Qy	601	GGCAGCGGCAGTACTTTTA	CATGAACAGGCGGAGGTGGATCGGCACCTCGAGTGCCTG	660			
Db	598	GGCAGCGGCAGTACTTTTA	CATGAACAGGAGGAGGTGACAGGCACCTACAATGCGCG	657			
Qy	661	GGTGGCGCATCTCGAG	CGCTCGCGCGCCCTGCGCGAGTGGCGGGGGCGGTGCG	720			
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Qy	721	TTCCGCGGCATCTCCGG	GGACCACTTGGAGCGGAGGTGGTGGAGCGCGCGCAGCTGTAC	780			

Qy	1861	CGCGTCTTACGTGCTCCTCGGCTTGGCGCCAGAGGCTTCACTCTGCCGACACC	1920	Qy	2941	TTTTACGACGATACCGTATCCGAGCGCGCGCGTATAGCCGAGCGCCCCGAGAGGAG	3000
Db	1858	CGCGTCTTACGTGCTCCTCGGCTTGGCGCCAGAGGCTTCACTCTGCCGACACC	1917	Db	2932	TTTTACGACGATACCGTATCCGAGCGCGCGCGTATAGCCGAGCGCCCCGAGAGGAG	2991
Qy	1921	CAGGGCGGTTTGGGGCTCGACAAAGAGCGGCCAAAGCGCCCGCGCTCTCGGGGG	1980	Qy	3001	TGCGTGGCGGACCCCTGCCGAGGAGACTGCGAGCGTTGGGGCGCTCTCTGCTAGAGCC	3060
Db	1918	CAGGGCGGTTTGGGGCGCGCGGGGAGGCGGCCAAAGCGCTCGGGCGCGAGCCCGGG	1977	Db	2992	TGCGTGGCGGACCCCTGCCGAGGAGACTGCGAGCGTTGGGGCGCTCTCTGCTAGAGCC	3051
Qy	1981	GAAGGGAGCGCGCGGGGACGGGAACGGGACGAGGATAGGACGACGAGGACGAG	2040	Qy	3061	CATCGCGCATCACCGACCGCGAGAGGACATCCAGGACTTTTCTCTCACCGCGCAACTG	3120
Db	1978	GACGAGGACGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2031	Db	3052	CATCGCGCATCACCGACCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	3111
Qy	2041	GACGGGACGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2100	Qy	3121	AGCAGACACCGCGCGCTGACACAAAGCGCTTGGCCACCTGACGCTGTATTACAAG	3180
Db	2032	GGGGCGAGCGGAGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2091	Db	3112	AGCAGACACCGCGCGCTGACACAAAGCGCTTGGCCACCTGACGCTGTATTACAAG	3171
Qy	2101	GGGGCGGGTCTCGACCCCACTTCGGGGTTTCACTGACCCCGCTGGTGGTGGTGG	2160	Qy	3181	CTCATGGCCCGCGCGGCGAGTCCCGTCCATCAAGGACCGGATCCCGTACGTCGTCG	3240
Db	2092	GGGGCGAGGCTTGAACCCACTTCGGGGTTTCACTGGAACCCCGCTGGTGGTGG	2151	Db	3172	CTCATGGCCCGCGCGGCGAGTCCCGTCCATCAAGGACCGGATCCCGTACGTCGTCG	3231
Qy	2161	TTTCCGAGCTGTACCCAGCATCATCCAGSCCACAACCTGTGCTTCACTAGCTCTCC	2220	Qy	3241	GCCAGACCGCGAGGTAGAGGAGACGCTCGCGCGCTGGCGCCCTCCGCGAGCTAGAC	3300
Db	2152	TTTCCGAGCTGTACCCAGCATCATCCAGSCCACAACCTGTGCTTCACTAGCTCTCC	2211	Db	3232	GCCAGACCGCGAGGTAGAGGAGACGCTCGCGCGCTGGCGCCCTCCGCGAGCTAGAC	3291
Qy	2221	CTGGGGCCGAGGCGCTCGCGCACTTGGAGCGGACCGGCACTTACCTGGAGATCGAG	2280	Qy	3301	GCCGCGCCCCAGGGAGACGAGCCGCCCCCAGCGCGCTTGCCTTCCCGGCCAAGCGC	3360
Db	2212	CTGAGGGCCGACGAGTGGGSCACTTGGAGCGGGCAAGGACTTACCTGGAGATCGAG	2271	Db	3292	GCCGCGCCCCAGGGAGACGAGCCGCCCCCAGCGCGCTTGCCTTCCCGGCCAAGCGC	3351
Qy	2281	GGGGCGGACGGCTGCTTCTGTAAGGCCACGTAACGAGAGCGCTGTGAGATCCTG	2340	Qy	3361	CCCGGGAGACGCGCTGCGATGCGGACCCCGGGAGGCGCTGCGAAGCCCGCGAAGCTG	3420
Db	2272	GGGGCGGACGGCTGCTTCTGTAAGGCCACGTAACGAGAGCGCTGTGAGATCCTG	2331	Db	3352	CCCGGGAGACGCGCTGCGATGCGGACCCCGGGAGGCGCTGCGAAGCCCGCGAAGCTG	3411
Qy	2341	CTGCGGACGCTGCTGCTGCAAGCAACAGCGCGCCCACTCAAGTGTGTGCACTCGG	2400	Qy	3421	CTGCTGCGAGCTGCGGAGGATCCCGGCTACGCGATCGCGGGCGCTTCCGCTCAAC	3480
Db	2332	CTGCGGACGCTGCTGCTGCAAGCAACAGCGCGCCCACTCAAGTGTGTGCACTCGG	2391	Db	3412	CTGCTGCGAGCTGCGGAGGATCCCGATCGCGATTTGCCACCGCGCTTCCGCTTGAAC	3471
Qy	2401	GAGGAGCGCTCTCTCGACAAAGCAACAGCGCGCCCACTCAAGTGTGTGCACTCGG	2460	Qy	3481	ACGGAATATTACTTCTCGCACTTGTGGGGCGCGCTGCGTACGCTTCAAGGCCCTGT	3540
Db	2392	GAGGAGCGCTCTCTCGACAAAGCAACAGCGCGCCCACTCAAGTGTGTGCACTCGG	2451	Db	3472	ACGGAATATTACTTCTCGCACTTGTGGGGCGCGCTGCGTACGCTTCAAGGCCCTGT	3531
Qy	2461	TACGGGTTACCGGGCGGACGAGTCTTCTGCGCTTCTGCGCTGCGTACGCTGCGC	2520	Qy	3541	GGAATAACGCGCAAGATACCGAGAGTCTGTTAAAGAGTTTATTCGCGAGAGCTGGC	3600
Db	2452	TACGGGTTACCGGAGCGGACGAGTCTTCTGCGCTTCTGCGCTGCGTACGCTGCGC	2511	Db	3532	GGAATAACGCGCAAGATACCGAGAGTCTGTTAAAGAGTTTATTCGCGAGTGGCAC	3591
Qy	2521	ACGACCATCGCGCGGAGTCTCTCGGACCGCGCGCTACGCTGACGCGCGCTGGCG	2580	Qy	3601	CCCCCGGAGAGCTGCGCGCGCTCAGCGCGCGGGTTCGGCGCGCGCGCGCGCGCG	3660
Db	2512	ACGACCATCGCGCGGAGTCTCTCGGACCGCGCGCTACGCTGACGCGCGCTGGCG	2571	Db	3592	CCCCCGGAGAGCTGCGCGCGCTCAGCGCGCGGGTTCGGCGCGCGCGCGCGCGCG	3651
Qy	2581	GAGTTGATCAGCTGCTGGCGGACTTTCGGAGCGCGCGGATGCGCGCGCGCGGTCG	2640	Qy	3661	GCTACGCGCGAGGAACTCTGTCGAATGTTGATAGAGCTTTGATACCTTAGCATGA	3717
Db	2572	GCTTTCGAAAGCTCTGGCGGATTTCCCGGAGCGCGCGGATGCGCGCGCGCGGTCG	2631	Db	3652	GCTACGCGCGAGGAACTCTGTCGAATGTTGATAGAGCTTTGATACCTTAGCATGA	3708
Qy	2641	TACTCCATGCGCATCATCGGGGACAGGAGTCCATTTTGTGTTTGTGCGCGGCGCT	2700	RESULT 10			
Db	2632	TACTCCATGCGCATCATCGGGGACAGGAGTCCATTTTGTGTTTGTGCGCGGCGCT	2691	AX358314			
Qy	2701	ACGGCGCGGCGTGTGGCGCATCGGCGACAGAGTGGGAGGACATCTCGCGCGGCTG	2760	LOCUS	AX358314	3708 bp	DNA
Db	2692	ACGGCGCGGCGTGTGGCGCATCGGCGACAGAGTGGGAGGACATCTCGCGCGGCTG	2751	DEFINITION	Sequence 5 from Patent WO0206513.	linear	PAT 13-FEB-2002
Qy	2761	TTCTCTCCCGGATCAGCTCGAGTGGGAAAAACGTTTCAACAGCTGCTCATCGCC	2820	ACCESSION	AX358314		
Db	2752	TTCTCTCCCGGATCAGCTCGAGTGGGAAAAACGTTTCAACAGCTGCTCATCGCC	2811	VERSION	AX358314.1	GI:18674962	
Qy	2821	AAGAAAAATACATCGCGGTCATCTGGGGGCAAGATGCTCATCAAGGCGGTGATCTG	2880	KEYWORDS	Human herpesvirus 1 strain KOS		
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Qy	2881	GTGCGCAAAACAACTCGGCTTTATCAACCGGACCTTCCAGGGCCCTGCTGACCTGCTG	2940	ORGANISM	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;		
Db	2872	GTGCGCAAAACAACTCGGCTTTATCAACCGGACCTTCCAGGGCCCTGCTGACCTGCTG	2931	REFERENCE	Alphaherpesvirinae; Simplexvirus.		
				AUTHORS	Homa, F.L., Wathen, M.W., Hopkins, T.A. and Thomsen, D.R.		
				TITLE	A method for treating herpes viruses		
				JOURNAL	Patent: WO 0206513-A 5 24-JAN-2002;		
				FEATURES	PHARMACIA & UPJOHN COMPANY (US)		
				source	Location/Qualifiers		
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[illegible]

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Db	3472	ACGGACTATTACTTCTCGCACCTGTTGGGGGGCGCGTGCATGACATTCAAGGCCCTGTTT	3531
QY	3541	GGAAATAAGCCCAAGATCACCGAGAGTCTGTTAAAGAGGTTTATTCCTCCGAGAGCTGGCAC	3600
Db	3532	GGGAATAAGCCCAAGATCACCGAGAGTCTGTTAAAGAGGTTTATTCCTCCGAGAGCTGGCAC	3591
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Db	3592	CCCCCGGACGACGTGCGCGCGGCTCAGGCGCGCGGGGTTTCGGCGCGCGGGGCGCGC	3651
QY	3661	GCTACCGCGGAGAACTCGTGAATGTTGCATAGAGCCTTTGATATCTTAGCATGA	3717
Db	3652	GCTACCGCGGAGAACTCGTGAATGTTGCATAGAGCCTTTGATATCTTAGCATGA	3708
RESULT 11	AB070847	Human herpesvirus 1 gene for DNA polymerase, complete cds,	
LOCUS	AB070847	3708 bp DNA linear VRL 03-AUG-2002	
DEFINITION	Human herpesvirus 1 gene for DNA polymerase, complete cds,		
ACCESSION	AB070847		
VERSION	AB070847.2	GI:18307581	
KEYWORDS			
SOURCE	Human herpesvirus 1		
ORGANISM	Human herpesvirus 1		
REFERENCE	1	Viruses; daDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.	
AUTHORS	Saijo,M., Yasuda,Y., Yabe,H., Kato,S., Suzutani,T., De Clercq,E., Niikura,M., Maeda,A., Kurane,I. and Morikawa,S.		
TITLE	Bone marrow transplantation in a child with Wiskott-Aldrich syndrome latently infected with acyclovir-resistant (ACVr) herpes simplex virus type 1: emergence of foscarnet-resistant virus originating from the ACVr virus		
JOURNAL	J. Med. Virol. 68, 99-104 (2002)		
REFERENCE	2 (bases 1 to 3708)		
AUTHORS	Saijo,M., Yasuda,Y., Kato,S., Suzutani,T., Morikawa,S. and Kurane,I.		
TITLE	Direct Submission		
JOURNAL	Submitted (30-AUG-2001) Masayuki Saijo, National Institute of Infectious Diseases, Department of Virology 1: 4-7-1 Gakuen, Musashimurayama, Tokyo 208-0011, Japan (E-mail:msaijo@nih.go.jp, Tel:81-42-561-0771(ex.791), Fax:81-42-564-4881)		
COMMENT	On Jan 23, 2002 this sequence version replaced gi:15408588.		
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ORIGIN

Query Match 82.3%; Score 3059.8; DB 14; Length 3708;
Best Local Similarity 89.3%; Pred. No. 0;
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ACCESSION

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KEYWORDS

Human herpesvirus 1

SOURCE

Human herpesvirus 1

ORGANISM

Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.

REFERENCE

AUTHORS

Saijo, M., Yasuda, Y., Yabe, H., Kato, S., Suzutani, T., De Clercq, E., Niikura, M., Maeda, A., Kurane, I. and Morikawa, S.
Bone marrow transplantation in a child with Wiskott-Aldrich syndrome latently infected with acyclovir-resistant (ACVr) herpes simplex virus type 1: emergence of foscarnet-resistant virus originating from the ACVr virus
J. Med. Virol. 68, 99-104 (2002)

JOURNAL

REFERENCE

AUTHORS

Saijo, M., Yasuda, Y., Kato, S., Suzutani, T., Morikawa, S. and Kurane, I.
Direct Submission
Submitted (30-AUG-2001) Masayuki Saijo, National Institute of Infectious Diseases, Department of Virology 1; 4-7-1 Gakuen, Musashimurayama, Tokyo 208-0011, Japan (E-mail: msaijo@nih.go.jp, Tel: 81-42-561-0771 (ex. 791), Fax: 81-42-564-4881)
On Jan 23, 2002 this sequence version replaced gi:15408591.

FEATURES

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ORIGIN

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 DEFINITION Sequence 7 from patent US 6682892.
 ACCESSION AR454710

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VERSION AR454710.1 GI:42688214
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 3708)
Homa,F.L., Wathen,M.W., Hopkins,T.A. and Thomeen,D.R.
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